

**FIGURE 1**

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA  
 CCTGGTGCACCACCACCA**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG  
 GTTTTCCACCCAGCTTTACCAAGGCCCTCCCTGTTGTGAAGAATTCATCACGAAGAATCA  
 ATGCTGTTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA  
 GAACTGGCCAAGAAGCTCAAAGAGGCAGCATTGGAACCATCGATGAAAAAATATTTAAAATT  
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA  
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT  
 ATGTC AAGGATAGAATTCATTCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT  
 TTGCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG  
 GGTGACAATTGGTGTGACCTTTGCGAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC  
 CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT  
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC  
 AGCTGGCATTTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCCAAGTAAAAAGTTTCTGA  
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTTGTGCTCATTTGGGATCTATG  
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT  
 AGTTCTTTTTCAGCATGTTCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT  
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT  
 ACATTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**GA**  
**A**AGTGACTCAGCTTCTGGCTTCTCTGTACATCAAATATCTTGTTTAAATGGGGCAGATATGC  
 ATTTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTGAAGATAAGAAACATGTCATCATA  
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTCTGGAGAATAAATGCAGT  
 AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT  
 TTGGTGAATGTGAAAACATAAGTTTGTGTGATGAGAATGTAAGTCTTTTTTCTACTTTAAAA  
 TTTAGTAGTTTCACTGAGTAACATAAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT  
 GCAGAATATTGTAATTAATGTCATAAGTGATTGGAGCTTTGGTAAAGGGACCAGAGAGAAG  
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTATTGATTA  
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCAATTT  
 GCTGAACTTAACAAAAGTGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG  
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC  
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA  
 ATAACCTTTAAACATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG  
 AATACAAACAGTATACTCATG

**FIGURE 2**

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL  
KEAALEPSMEKIFKIDQMGRWFWAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI  
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGCTCTCCGCCTTCTGCAT  
 CGCGGCTTCGGCGGCTTCCACGTAGACACCTAACAGTCGCGGAGCCGGCCGCTCGTGGAGG  
 GGTCCGCACGGGGAGTCGGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTGCGAAGATGTCGG  
 ACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCAGCGCTATTGGTTCGCCGCCACCGCTC  
 CGCGTGCCTTGGTCCGCAAACTCGGCCTCATCAGCCCGGCCCTACCTCTTCCCTCTGGCCCCGA  
 AGCCTTCCCTTATCGCTTTTCAAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG  
 GTCCAGGAACCTGGATTTCTTATTTGGTCAATTTATATTTCTTATATCAGTATTTCTACGCCGA  
 CTTGAAACAGGAGCTTTTATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG  
 GATTTCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCTCTGATCA  
 TGTCAGTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA  
 ACACGATTTAAGGCTGCTATTTACCTGGGTATCTCTTGGATTCAACTATATCATCGGAGG  
 CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCCCTAATGTTCGA  
 GATACCCAAATGGACTTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG  
 CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCTCTGCTAGCATGAGGCGAGC  
 TGCTGATCAGAATTGGCGGAGGCCGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC  
 AGTGAAGGGCGGCTCGGCGCCGCTCCTCTCAAGCCACATTTCTCCAGTGTCTGGGTG  
 CACTTAACAACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACTGAATGTAGTCTTTC  
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCACAAAGTTTACAGAT  
 TCTCATTCAAGTCCCTTACTGCTGTGAAGAACAATAACCACTGTGCAAAATGCAAAATGAC  
 TACATTTTTTGGTGTCTTCTCTTCTCCCTTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTCT  
 AATCTGCTGGCATTGAGCTGGGGCTGGGTCAACAAACCTTCCCAAAGGACCTTATCTCTT  
 TCTTGCACACATGCTCTCTCTCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG  
 CCAATAAAATTGCTCTGCCCTTGACAGGTTCTGTATTATTGACTTTTGCCAAGGCTGGTC  
 ACAACAATCATATTCACGTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGGAG  
 AAGACAGCCACGGATGAAGCGTTTTCTCAGCTTTTGGAAATGCTTCCGACTGACATCCGTTGTT  
 AACCGTTTTGCCACTCTTTCAGATATTTTTTATAAAAAAGTACCCTGAGTTCATGAGGGCCA  
 CAGATTGGTTTATTAATGAGATACGAGGGTTGGTGTCTGGGTGTTTTGTTTCCCTGAGCTAAGTGA  
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC  
 TTTGCGTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTGGGTTGCTTTGTGT  
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTTCTGGGCATTG  
 ATTCCCATTTCAATCTCATTTCTGGATATGTGTTATTGAGTAGTAAGGAGGAGACCTCATA  
 CGCTATTTAAATGTCACTTTTTTTGCCTATCCCCGTTTTTTTGGTCTGTTTTCAATTAATTGT  
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTTAAAGCTAATGTAAGCACATCTA  
 AGGGAATAACATGATTTTAAAGTTGAAATGGCTTTAGAATCACTTTGGGTTTTGAGGGGTGTGTTA  
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT  
 TCGTAGGTGGGCTTTTCCCTATCAGAGCTTGGCTCATAACCAAATAAGTTTTTTGAAGGCCA  
 TGGCTTTTCCACACAGTTATTTTTTTATGACGTTATCTGAAAGCAGACTTTTAGGAGCAGT  
 ATTGAGTGGCTGTCACACTTTTAGGCAACTAAAAGGCTTCAAACGTTTTGATCAGTTTCTT  
 TTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTTCCCCACTCTTAAACAGTGTGAT  
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG  
 TACTTCTCCATATTTAATTTATATGATAAAATAGTGGGAGAGTCTGAACCTTAACTGATCA  
 TGTTTTGTGTTTCATCTGTGGCCACAATAAGTTTACTTGTAAAAATTTTAGAGGCCATTACT  
 CCAATTTATGTTGCACGTACACTATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATA  
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCCTCTACAGTCAGCTGCTGCCGAG  
 CAGTCATTTTTTCTTAAGGTTTACAAGTATTTAGAACTTTTTCAGTTACAGGCAAAATGTTT  
 ATGAATTTATTCCTTTAAACATGGTTTAGGAAGCTGATGACGTTTATGATTTTGTGTGGATT  
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTGAGTTTTGACTTGACAAAGCAAAACA  
 TGACGTGGATTCTCTTTTACAAATGGAAAAAAAATCTCTATTTTGTATAAGGACTTCCC  
 TTTTTGTAACTAATCCTTTTTTATTGGTAAAAATGTAAATTAAATGTGCAACTTG

## **FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGSLSPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGGRFL  
GDQ

### **Transmembrane domain:**

amino acids 98-116, 152-172

### **N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

### **Glycosaminoglycan attachment site.**

amino acids 218-222

**FIGURE 5**

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAAC TG GTT G  
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCTACTCCCTCTCGGCT  
 CCTTGTGGCCCAAAGGCCTAACGGGGTCCGGCGGTCTGGCTAGGGATCTTCCCCGTGCCC  
 CCTTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG  
 CGGGGTTCTCGGAGGCCAGACTGGTCCATCCCCATCTTGGACTTGTGGAACAGAAATGT  
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT  
 GGCTGTGTTCCCTTGTTTGTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC  
 ATCAGGAATACAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT  
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC  
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA  
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT  
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAATCCT  
 GAGGGAAGTTCTTAGAAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGGAAAA  
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG  
 AATAATTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCCTCAGAAGTTAAATGCATTT  
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCTCCCTCC  
 CACAAAAAGGCCTGAAGATTCCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC  
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA  
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG  
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAAACTCAAAGAAGAAGTTATTAATA**AGTA**  
**ATA**ATTAAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC  
 CTTACACTG

**FIGURE 6**

MAAEEEEDEVVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP  
 LVFDDEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP  
 VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVDLEHEEMKILREVL  
 RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFHAPPSEVKMHFANQS  
 IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS  
 MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRLLAEKLEEVIK

**N-glycosylation sites.**

amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**

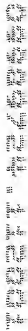
amino acids 273-279

**Amidation site.**

amino acids 252-256

**Cytosolic fatty-acid binding proteins.**

amino acids 78-108



**FIGURE 7**

GGGCACAGCACATGTGAAGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG  
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAAT  
CCTGAGGGAAGTTCTTAGAAAAATCAAAGAGGAATATGACCAGGAA

**FIGURE 8**

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG  
 TAGCTTCTCCACGTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTCTGAGGGAGGTAATTAAGAAC  
 AGTGGAATGGAAGAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC  
 ATTCCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT  
 CTGCCAATGAAGAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTG  
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG  
 AAATTTGAAATATGCTTCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTGCCT  
 TTCTTTATTTCTCGGATAAATTGATTGCTTCTATGTCTCTATCTTCAACCAGCCATG  
 GCTGTTATCTTCTCAAATTTTAGCATTATAACACAGCTCTTCTATTACAGGATAGTGCTGAA  
 GAGGCGTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT  
 TGACTGCCGGGACTAAAACCTTACAGCACAACCTTGGCAGGACGTGGATTTTCATCAGCATGCC  
 TTTTTCAGCCCTTCCAATTTCTGCCTTCTTTTTCAGAAGTGAGTGTCCCGAAGAACAAATG  
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC  
 ACATCCGTCTTGGCATGGGCCATGTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT  
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA  
 GAACAGCAAACTCTATTTCTTTGGCATTTCTGTTTAATGGGCTGACTCTGGGCCCTTCAGAGGA  
 GTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC  
 CTTATTTTTGTAAGTGCATTCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAA  
 CATGTTCCATGTCTTGATGGCCAGGTTACCAGTGTCTTATATACACAACAGTGTCTGTCTCGG  
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCTCTCTCTCTATA  
 TTTATTTATAATGCCAGCAAGCTCAAGTTCGGAATACGCACATAGGCCAAGAAAGGATCCG  
 AGATCTAAGTGGCAATCTTTGGGAGCGTCCAGTGGGGATGGAGAAGACATAGAAGACTTA  
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGGTACCCACATAGATTTTGA  
 GCTCTCTTGAACCTTATTTTCACATTTTCAGTGTGTTGAATATTATCTTTTCACTTTTGATA  
 AACCAGAAATGTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT  
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCAAAGAACTGATACAGGAGTAACA  
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCGAGATTAT  
 TTTCTTGGCCCTTCAAGCTTCCAAAAAAGCTTGAATAATCATGTTAGCTATAGCTTGTATAT  
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT  
 CTTCCCTTTTTAACATTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGT  
 CATTTTGCAAGTAAAGAGCAACGGGACCCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC  
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGTGCTGAAGAAGCAGT  
 TTCTCAGACACAACATCTCAGAATTTTAAATTTTGAAGAAATTCATGGGAAATTTGGATTTTGT  
 AATAATCTTTTGATGTTTTAAACATTTGGTTCCCTAGTCACCATAGTTACCAGTGTATTTTA  
 AGTCATTTAAACAGGCCAGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT  
 GTCATTACTCTGAATTTATACATTTTGGAGAATAAGAGGGCATTTTATTTTATAGTTPACT  
 AATTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC  
 CAGATTGTCAGTGAAGCTGATGCCTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT  
 AGCAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC  
 AGTAATATATAAGTCACCTTTACAGTGTACTTTCACACTTAAAGTGCATGGTATTTTTTCATG  
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAAGGTGATAGATGATATTA  
 AAATTAGCAAAACAAAGTGACTTGTCTCAGGGTCATGCAGTGGGTGATGATAGAAGAGTGGG  
 CTTTAACTGGCAGGCCCTGTATGTTTACAGACTACCATACTGTAATATGAGCTTTATGGTGT  
 CATTCTCAGAACTTATACATTTCTGTCTCCTTTCTCCTTAAGTTTCATGCAGATGAATATA  
 AGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAAATTG  
 GTGGAAATTTGTAATTAATAATTATTAACCT

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**FIGURE 9**

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK  
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV  
IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF  
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTTLGLQRSNRDQIKNCGFFYGHSFAFSVALI  
FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVITTVSVLVDFRPSLEFFLEAPSVLLSIFI  
YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLT KPKSDESDEDTF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
298-318, 328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

**FIGURE 10**

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG  
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCCTGCCTTTCTTTATTTCC  
TGGATAACTTGATTGCTTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGCTGAAGAGGCGTCTAAA  
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAACTTTA

GGACGCGTGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGCGGCC  
TGGCTAAGGCTGCTCAAGCGAGCCTTGGGAGAGCAGCGGCTCGGGGACAGAGGACAT  
CCGCTCTACAGGTTCCAGGCGGCTGGCCCGGGCTATGCGCAAAGGAGAGCGCCGAG  
AGCGGCTCCGCGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCGCGGCCA  
GGTGAAGAAAGAACGAAAAAGAAACAAAGATGTCTGTTTGCACAAGCTTTGCTATG  
CACTTGGGGGACCCCTACCAAGTGACGGGCTGTGCCCTGGGTTCTCTCCTTCAGATCTAC  
CTATTGGATGCTGGCTCAGGTGGGCGCTTCTCTGCTTCATCATCTGTTTGTGGCGGAG  
CTGGGATGCCATCAGACAGCCCTTGTTGGGCTCTGCATGACAAATCCCCCTGGACCTGCC  
TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCGCCCTGGCGCTATTGCCCTACTTCTCT  
ATCTGTTTCTGCGCGACTTCCCACAGCGCAGACCTATTGGTACCTGCTTTTCTATTGGCT  
CTTTGAACAAATGGTGCAGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA  
ACCGAGCAGACTGAGCGGGATTCTCGCCACCGCTTATCGGATGACTGTGAAGTGTGCGGCAC  
AGTGTGGGACGGCGATCCAGGACAAATCGTGGGCCAAGCAGACAGCCTTGTTCCTCAGG  
ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAAACCATACACATGGCACCACCTTCACAC  
AGGAAAGACGAAAAGGCATACCTGCTGGCAGCGGGGTACCTGTGTATCTATATATCTG  
TGCTGTCACTCTGATCTGGCGCTGGGGAGCAGAGAACCTTATGAAGCCAGACCTGT  
AGCCAATCGCCTACTTCCGGGCGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCT  
TTATCTGGCTTCTTCTCACTCTCTGGCTTTCATGCTGGTGGAGGGAACTTTGCTCTTGTT  
TTCACCTACACTTTGGGCTTCCGCAATGAATTCAGAATCTACTCTCGCCATCATGCTCT  
CGGCCACTTTAACCATTTCCCATCTGGCAGTGGTTCTTGACCGGGTTGGCAAGAAGACGCT  
GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCACTTGGTGGCCCTCATGGAGAGATAA  
CCTATCATTTACATATCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC  
TACCCTGGTCCATGCTGCCTGATGTTCATGTACGACTTTCATCTGAAGCAGCCCACTTCCAT  
GGAACCGAGCCATCTTCTTCTCTCTATGTCTTCTTCCACCAAGTTTGCTCTGGAGTGT  
ACTGGGCATTTCTACCTCAGTCTGGACTTTGCAGGTTACGAGCCCGTGGCTGCTCGCAGC  
CGGAACGCTGTCAAGTTTACATGAACATGCTCGTGACATGCTCCCATAGTTTCTCATCTCT  
GTGGGCTGCTGCTCTTCAAATGTACCCCAATGATGAGGAGAGGCGCGGCCAGAATTAGAA  
CGGCTCGAGGCACTGAGGACGAGGCGCAGCACTGTGGCTGCTCAGAAACAGACTCCACAG  
AGCTGGCTAGCATCTCTTAGGGCGCGCCACGTTGCCCGAAGCCACCATGACAGAGGCCACAG  
AAGGCTACAGGACTGCTTGC CGGCTGTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
CTGAAGACTCAAGGAGTGGCCCGCAGGACACTGCTGCTCACTGTGGGCGCGGCTGCTCTG  
TGGCTCTGCTCTCCCTCTGCTGCTGTGGGGCAGGCTGGGCTGCCATGCACTGTGTAATA  
TGCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC  
TAATTAATAACTTAATGACTGTGTGTACATAGCAATGTGTGTATGTATATGTCGTGAGCTA  
TTAATGTTTAAATTTTTATAAAGCTGGAAGG

MWLRWALSLPSSCLWAEPMGPSQTPWWASASANPPGPAWVALCPGSSSRPWPSPLTSSSG  
SCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCCSATEQTERDSATAYRMTVEVLGTVL  
GTAIQGGIVGQADTPCFQDFNSSTVASQSANHHTGTTSHRETQKAYLLAAGVIVCIYIICAV  
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCT  
YTLGRFNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNLMLVTMAPIVLILGLLLFKMYPIDEERRQNKKAL  
QALRDEASSSGCSETDSTELASIL

**FIGURE 13**

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT  
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA  
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT  
TGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCAT

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**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT  
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT  
 GGTGGTTTCAGCAAGGCCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
 CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA  
 GAGAACGTTATCATCAAATTAAACAAGGCTGGCCTTGTAAGTACTGAGTTGTTTAGG  
 ACTTCTATTTGTGGCAAACTTCCAGAAAACAACCTTTTTGCTGCACATGTAAGTGGAGCTG  
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCACCAAATG  
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
 AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG  
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT  
 ACTGCAGCAGAAATGGTCTATGTCAATTTCTTCTTGGTTTTTTCTGACTTACATTCGTGA  
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG  
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT  
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA  
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA  
 TTAAAAACACCTATGCCTATACTTTTTATCTCAGAAAATAAGTCAAAAGACTATG

**FIGURE 15**

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AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG  
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG  
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYD  
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**FIGURE 16**

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT  
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA  
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAACAGAAAACCTGTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC



**FIGURE 17**

CCCACGCGTCCGCCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG  
 CCGGGGTGCGGAGCCGAC**ATG**CGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC  
 CTTGCGCTTGTACTTGTGTGTCACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG  
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG  
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCCTACGTGTTCTGCTCTTCTGCGGCGCCTA  
 CCTCTACAAACAGGGCTTTGCCATCCCCGCGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT  
 TGTTTGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC  
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT  
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT  
 TGAGACTTTTCCCCATGACACCAAAGTGGTCTTGAACCTCTCGGCCCCAATTCTGAACATT  
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTATCTGTGT  
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG  
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAATAAATTT  
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA  
 CACA**TGAT**TCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA  
 TGTGGTCTCTAAAGCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG  
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT  
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT  
 GGCCGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC  
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT  
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC  
 AGGAGAATTGCTTGAAACCAAGGTGGCAGAGGTTGAGTAAGCCAAGATCACACCACTGCACT  
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

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MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSPDLAELRELSEVLREYR  
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLGALFGPWLGLLLCCVLTSGATCCYLLSS  
IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMPNPWFLNLSAPILNIPIVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ  
LNETSTANHIHSRKDT'

Signal peptide:

Transmembrane domains:

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

### Protein splicing proteins.

amino acids 25-31.

## Sugar transport proteins.

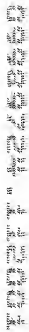
amino acids 162-172

**FIGURE 19**

CCGAGGCGGGAGGAGCCCCGAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT  
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAA  
 TAGGAAAATAACTTGGGATTTTATATTGGAAGAC**CATG**GATCTTGCTGCCAACGAGATCAGCA  
 TTTATGACAACTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG  
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC  
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
 TGCTCACTGCCTACTTTGTGATCAACCTTTCAGCCATTAGCACCTGAGCCAGTGCTTTTCT  
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA  
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC  
 CAGACTTGAACCCCTGGTGGACAAACGACTGTGAGCAGAAATGAGTCAGAGCCCATTCTCTGCC  
 AACTGCACTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA  
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATTC  
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG  
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA  
 CAGATCACAAATGTTACGTGAGCTTTTTCCTGTTTTCACTCACCTGCCATTTCCAAAAGATG  
 CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA  
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCTG  
 ACACCACCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
 GGAACGCTTTCTCAGAACTG**TAG**GAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGA  
 AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAACTGCAAAA

**FIGURE 20**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY  
KVLATLGLILLTAYFVIQPFSPLAPEFVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPYPWRRLNRSQMLRELFV  
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQRRHCQSVAMP  
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL



CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG  
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC  
AAGGGACACGTGGTTTTCCGAACAGCTCAGAATAGGAAAAATAACTTGGGATTTTATATT  
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTTCAGAGACTGTTG  
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGCAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAAAAGATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT  
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC  
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

**FIGURE 22**

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
 CAGGGTCCCCACTTGCAGTCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGGCTGGTG  
 CCACTGGTGGCGACGCTGCTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGGACTGCC  
 CTCCCTGCCACCCACCAATTGGCAGCCCCACCTTCTTTGAAGACTTCCAGGGCTTTTTGTGCCA  
 CACCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAACTGATCCCAAGTTCGAAAATG  
 GACACGATATGCTAAGAGCCACGACCTTATGTGAGTTTCTGGAATGCCTGCTATGACATGCT  
 TATGAGCAGTGGGCGAGCGGCCAGTGGGAGCGCGCCAGAGTCTGCGGGCTTCCAGGAGC  
 TGGTGCTGGAACCTGCGCGAGAGGGCGGGCGCCCTGGAGGGGCTACGCTACACGGCAGTGCTG  
 AAGCAGCAGGCAACGCGAGCACTCCATGGCCCTGCTGCACCTGGGGGGCGCTTGGCGCCAGCT  
 CGCCAGCCCATGTGGGGCTGGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGTCCA  
 GCGCCGAGACATATTACCGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTCAC  
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCGAGGAGGC  
 CTCACCTGCTCTGGCAGTGACCAAAGAGCCAAAGTGAGACCCCCACCCGAGTTGCTGCGAGG  
 AGGACGAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGGAGGCAGCAGAATG  
 GATGAGAGCGCTGAGAAGCTGGTGTCTGCGCCGAGTGCCAGCTGGTGACGCTAGTGGCCGT  
 GGTCCCAGGCTCTGAGGCTCACCACACAGAATGTATACTTACGATGGCAGCTGAGCGTAGC  
 GCGTGGAACCGAGGAGGCGATCGGCTATGATTTCCGGCGCCCATGGCCAGCTGCGGTGAG  
 GTCCACTGCGCGGTTTCAACCTGCGCGCTTACGACTTGAGCTTCTCTTATCGATCAGGC  
 CAACACTTCTCAACTTCCCATGCAAGTGGGCGACGACCCAGCTCATCTCTAGCCAGA  
 CTCGAGAGCCCCAGCCTTGCCCCATCCACCCCCATACCCAGGTACGGCAACGAGGTGTACTCG  
 TGGCTCCTGCGCTTACGGCCCCCTCTCAAGGCTACCTAAGCAGCGCTCCCCCCAGGAGAT  
 TGTGCGTGCCTCAGGCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAATTCGAGTACT  
 TGATGCAACTCAACACCAATTGCGGGCGGACCTACAATGCTGTCTCAGTACCCCTGTGTTT  
 CCCTGGGTCTGCGAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCCGTGTCCG  
 GGACGTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGAGAAGT  
 ATGAAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCCACTATGGCACCCACTACTCC  
 AATGACAGAGGCGTGATGACACTACCTCATCCGCGTGGAGGCCCTTCACTCCCTGACAGTCCA  
 GTTGCAAAGTGGCCGCTTTGACTGCTCCGACCGGACGTTCCACTCGGTGGGGCGAGCCGTGGC  
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATCTTCTAGTTTCCCT  
 GACTTCTTGGAGAACCAAGACAGCGTTTGTGACTGGGCTGTCTCCAGTGACCAACGAGAAGGT  
 AGGCGATGTGGTGTACCCCCGTGGGCCAGCTCTCTGAGGACTTCATCCAGCAGCAGCCGCC  
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC  
 TACAAGCAGCGGGGGCGAGCCGCGAGGAGGCCCTCAATGTCTTTATTACTGCACTATGA  
 GGGGCTGTAGACTGGACCATGTGACAGATGAGCGGGAACGAGGCTCTGGAGGCAATTA  
 TCAGCAACTTTGGGCGAGCTCCCTGTGAGTGTGAGGAGCCACATCCAACCTCGGCTCTCA  
 GCTGGAGGAAGCAGCCCATCGCCTTGCAGCGCTGGACACTAATCAGCTAGCATCTTCCAGCA  
 CCTGGAGCAACTCAAGGCATTCTTCGACAGAGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAGACCCCC  
 ACCATGGGCGACCCACAAGACGCGAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCGAGTGGTGT  
 GAGTGGACAAGCACTGGCAGTGGCCCCGATGGAAGCTGCTATTGAGCGGTGGCCACTGGG  
 ATGGCAGCTGCGGGTGAATGCTGACTACCCGCTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC  
 CTGTGATGTAGTAACCTGCCTTGCATGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG  
 GGACACCGCTGCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGAGTGGCCATCAGCACT  
 CAAAGCTGTGCGAGTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT  
 GAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAACCTGTGATCATACACACTGTACGCCG  
 CGGACAGTTTGTAGCGGCACACTACGCCCTCTGGGTGCCACATTCCTGGACCTATTTTCCACC  
 TGGCATTGGGGTCCGAAGGCCAGATTTGTGGTACAGAGCTCAGCGTGGGAACGTCCTGGGGCC  
 GTGACTACCTACTCTTGCATTTGATTTAGTCAATGGGAAGTGTGGGGCTTCACTGTCCCTT  
 GGCAGAGCAGCTTACAGCCCTGACGGTGACAGAGACTTTGTGTTGCTGGGCGACCCGCCAGT  
 CGGCCCTGCACATCCTCAACTAAACACACTGCTCCGCGCGCGCTTCCCTTGGCCATGAAG  
 GTGGCCATCCGACGCTGGCCGTGACCAAGGAGCGCAGCCAGCTGCTGGTGGGCCGTGGAGGA  
 TGCAAGCTCATCTGTGGTGTGCGGGGCGAGCCCTGAGGTGCGCAGCAGCAGCTTCCGCG  
 GGAAGCTGTGGCGGTCTCGCGCGCATCTCCAGGTGTCTCGGGAGAGCAGGAATACAAC  
 CTTACTGAGGCGCGCTGAAGCTGGCCAGTCCGGCTGCTCGGGCCCCGCCCCGGCAGGCCGT  
 GCGCGGAGGCCCCCGCCAGAAGTCGGCGGGAAACCCCGGGTGGCGAGTGGCGGGGTGA  
 GCGGGGCCACCTTGCACGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG  
 GCGGAAGTCCCCCCCCTCGCCGCTGAGGGGCGCCCTGAGGGCCAGCACTGGCGTCT

**FIGURE 23**

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNP  
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETP  
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVFYFDGSTERVETEEGIGYDFRRP  
 LAQLREVHLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV  
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL  
 SQYPVPFPVWLQDYVSPTLDLSNPAVFRDLSPKIGVNVNPKHAQLVREKYESFEDPAGTIDKFH  
 YGTHYSNAAGVMHYLIRVEFFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLESADVKELIP  
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDDVLPWASSPEDFIQQHRQALESEYVSAHLHEW  
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDNTNSPISIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPTMGSHKTQRLLSGFWVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRTALPRGKLL  
 SQLSCHLDVVTCCLALDTCGIYLISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS  
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA  
 WERPGAQVITYSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLGDKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS  
 GETEYNPTEAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
 CACGGCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT  
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC  
 TGGACCCCTTAACGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT  
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC  
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG  
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC  
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC  
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTCGTCCTGGACAAAGTCACAGA  
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTCTCTTTT  
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC  
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT  
 TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG  
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC  
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT  
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG  
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC  
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCAGCTAC  
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA  
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAAACAAAACAAACAA  
 AAAGATTTTATTAAAGATATTTTGTTAACTC



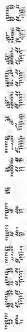
RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGF  
WTLNWVLALGQCVLGAGAFASYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFAGALITLVQ  
IARVILEYIDHKLGRVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNKNCVSAK  
NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVVGVGVLSEFFFFSGRIPLGKDFKSPHLNYY  
WLPIMTSLGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKLILGKKN  
EAPPDNKKRKK

**FIGURE 26**

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGT  
 GGCT**ATG**TTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC  
 TTCTCTTCGTGGCTCGGACGTGGATGCTCTGTGTGCGTGCAGATCCTTCAGGCCTTGTTT  
 CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC  
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG  
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG  
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA  
 TGACCTTGAAGTTCCCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACAGGTTAGAAGAGGAGATA  
 GTGGAGCAAACCATGCGGAGGAGGCGAGCGGAGAGTGGGAGGCCCGGAGAAGAGACATCCT  
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG  
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC  
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTTCGACGG  
 CCACGTTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA  
 CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGTCTACCAGCACTGGTCCCTCCATGAC  
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
 GCGGCTCCAGGAGTTCTTGCAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC  
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA  
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTATTTGGGTTCAAGCACAAAGTT  
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT  
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
 TACCATGGCCTGGAACTCGCCAAGAAGCAGCTGCGAGCCACCAGCAGACCATTGCCAGCTGC  
 CTTTGACCAACCTCGTCATCTCCAGGGCCTTTTCTGTACTGCTCTCTCATGGAGGGCAC  
 TCCAGATGTCATGCTGTTCTCTAGGCCGTCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
 AGTCCTTTGTGTGTTTCGACAAAGAACCGGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC  
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC  
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA  
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
 CTGGACGCACCTATTTCCCTCCTGTCC**TAGGA**AATTTGATTCTTCCAGAATGACCTTCTTATT  
 TATGTAACCTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT  
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

**FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETA  
LEHKEQFHYFILINCGANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAIEDIFRDEEEDDEHSGNDSGSEPSEKRTRLEEEIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH  
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR  
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL  
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKQLRATQQTIASCL  
CTNLVISQGPFYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP  
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL  
DALISLLS



STACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCAGTTTCTGGGTGGCAAGAACTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC

CAGGAAGCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC  
 CACGAAAGGACGATACCGAAAAACACCTCAACCACAAAGGAAATAGACTACAGCCCAATTG  
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAAGCAAGAAAGAGACAGCTTTTTTTTGGAAAGCTAA  
 GTCTTCCCTTTATTCGAGTCAAGAAACCCCTCTCTTGAGCTATTTCAGCTTTTAAACAAAT  
 GAGTAAAGTAGCTGTCGGGTCACT**CGTGGT**GACAGCGCCCTGGGTCCCGCTCGGGCAGCGCTC  
 CTGCTCTTTCTCCTGATGTGTGAGATCCGATATGTGGAGCTACCTTTTGACAGAGCTGTGGC  
 CAGCGGCTGCCAAGCGGTGCTGTGACTCTGAGGACCCCTGGATCTGCCACTGTATCTCTCA  
 CCTCTTCTCCCGGCCGCCACCGCTGCTTGAAGTACAGACCTACATTATATACCCATC  
 CTGAAGGTGACAAGAGGGGACCCAGGCCCATGGCCCTGCCAGGTACATGGGCAGGAGG  
 TCCCCAAGGGGAGCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGGCCG  
 GCGCCCGCTGCGCAAGAGCGCTTTCTGCCCTTCTCAGTGGGCGCAAGACGCCCTGCACAGG  
 GCGAGGACTTCCAGAGCTGCTCTCTTGAAAGGGTCTTTGTGAACCTTGATGGGTGCATTGTGA  
 CATGGCGACCGCGGCACTTTGCTGCTCCCTCGCTGGCATCTACTTCTTCAGCTCAATGTGC  
 ACAGCTGGAATTACAAAGGACGATCGATGCACATTATGATACACCAAGAAAGAGCTGTCATC  
 CTGTACGCGCAGCCGACGAGCGAGCGATCTATCAGAGCCAGAGTGTGATGTGCTGGACCTGGC  
 CTACGGGGAGCCGCTCTGGTGGCGCTTTCAGCGCCAGCGGAGAACGCCATCTACAGCA  
 ACGACTTGCACACCTTACATCACTTTCAGCGGCCACTCATCAAGGCCGAGGACGACT**GA**GGG  
 CCTCTGGGCAACCTCCCGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG  
 TTTGCACTGCTGTGAAGCAGGAAGAGCCAGGAGGTCCCGGGGACCTGGCATCTGGGGAGA  
 CCTGCTCTATCTTGGCTGCTCATCTCCCTCCAGCTATTTCTGCTCCTCTCTCTCTCTCT  
 TGGACTATTTTTAAAGAGCTTGCCTTAACATAAATATTGTAGAATTTGCCAGCTCTGTAGCT  
 AGCACTCTCAAACTTGAATAATGCATGCAATACCCCGGGGTTGCTGTAAATCGAGATTCT  
 GACTCAGCAGGCTGTAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGTG  
 ATGGGCTCAGTCTTATGAACACACATGGAGCAACAGGTTCTTAGAGCTTTCTCAATATTCTAG  
 TACTTTCTGAACATTCTGGAATCTCCCAACATTAGAACTTCCCAACATTTTTTTCTC  
 TGAGACAGACTTTGCTCTGTTGGCCAGCTCAGATGCAAGTGGTGAATCTCAGTTCACTGCA  
 AACCTCTGCTCCCGGTTTCAAGCGATTCTTCGCTCAGCTCCCTAGTGCTGGGTATAC  
 AGGCGCTGCTACCATGCTCGGTCAATTTTGTATTTTTAGTAGAGATGGGGTTTACCATA  
 TTGGCCAGGCTGGTCTGAATCTCTGACTCAGGTAGCCCAACCCGCTCGGCCCTCTCAAAAT  
 GCTGGGATTACAGGTGTGAGCCACGCTGCTGGCCAAATCCAACATTCTAAATCTCTCAT  
 CCTCTCGAGGGCTCCCGTGCTATGTGTTCTTACCCCTTCCCTCTCTCTCTCTCGAGCC  
 TGACCACTCGAGCCACCGTTCTATTATTATTCATTATAAACCATGAGCACTACTCTGTGCT  
 GGGTCCCGGGAAGGGTGAGGGGTGCAGACAGGCCCTCGCCCTGCCCTCAGTGACTGCGCCA  
 GTCAGCCAGCGCGGGGAGAGATGTGTACATAGTTTAAAGCAGACCCAGACTCATGGG  
 GCTGTGTTCTGGTGTTTCAAGTGTGCTGGTCTCTCCATTACCACTGCTGCCCAAGGCTGG  
 TGGGACGGGTCCGGTGGCAGGGGCAAGTATCTCTCCCTTCTCATCCAGCTGCCAC  
 TGCTCATCTGTACAGCAAAACCCAGGGGGCTTGGCAGGTTCAAGGGTTCTGTGTAGGAGG  
 ACCCAGGAGTGTGGGGGCAATTGGGGGTGAGGTGGCCCGGAAGAAATGGAACCCACACCCA  
 TAGCTCTCCCCACAGCTGATACGGCATCTCGAGAGAAGCCCTGCCCTCTCATGGGATCCC  
 CTCTCTGCTCTCTCCAGGGCTCTGCCAGGGCTCTGCTCAGTCCCTCCACCAAGGATCATCT  
 GAACCTTCGGTTTCCCCAGGGCTCCAGCTGCCCTCAGACACTGATGTCTGCCCCAGGTGCT  
 CTCTGCCCTCATGCCCTCTCCAGCGCCAGTGCAGCCGACTCTCAGGCTTTATCAAGGTT  
 CTAAAGCCCGGGTGGGAGCTCTCTGCTCAGAGCCCTCTCGGCCCTGGTGTCTGCTTTAC  
 AAACACCTGCAGAGAGAAGGGCCAGGGAAGCCAGGCTTTAGAGCCCTCAGCAGGTTCTGGG  
 AGCTAGAGCAAGGAGGACCTCAGGCTCTCCGTTCTTCTTCCAGGTTGGGTGGCTGGT  
 GTTCCCTTAGCCTTCCAACCCAGGTGGCTGCCCTTCTCCCAAGAGGAGGGCGGCTCCGC  
 CCAATTGGTGCTCATGACACTCTGGGGCTGAGTGCGCCCGGGGGTGATCTCTGGTGTCTAC  
 AGCCGAGGAGGCTGCTGCTTCATGGCCAGATGACGGAACAGGCTCTGACCAGTGGCAGGA  
 AGACTGTGCTATAAACACCCCTGCTCATCTTCTGCCCTGCTCTGACCCCGCAGCCGCTGCC  
 GTCCAGCATGATTAAAGAATGCTGTCTCTCTCTTGGAAAAAATAAAAAA

**FIGURE 30**

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDLDPAHVSSASSSGRPH  
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGEPGQSGKDGKMGSPGAPCQKR  
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET  
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT  
FSGHLIKAEDD

**Important features:****Signal peptide:**

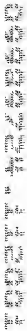
amino acids 1-20

**N-glycosylation site.**

amino acids 72-75

**C1q domain proteins.**

amino acids 144-178, 78-111 and 84-117



**FIGURE 31**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGACCCGCCAGGAAAGACTG  
 AGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCGCTCCCGGGACAGAA**ATG**TG  
 CTCCAGGGTCCCTGCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG  
 GCTGCCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG  
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT  
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTAC  
 AGAACCATGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCAACCTCAGCAACCTG  
 GACCTGACGGCCACAGGCTGCATGAAATACCAATGAGACCTTCCGTGGCCTGCGGCGCCT  
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCTTTCGACACGC  
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCGTGC  
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT  
 CCTGGACATGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG  
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCGACAACAGCTGGAG  
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCCTGGGCTGGCCGGCAACAC  
 CCGCATTTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATG  
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCCTGCGG  
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCTG  
 GGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA  
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCAGCTTTGGCTGCCAGCCACCACC  
 ACCACAGCCACAGTGCCCAACGAGGCCGTGGTGCGGAGCCACAGCCTTGTCTTCTAG  
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCGCGCTTCCA  
 CTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC  
 AATGGGGGCACATGCCACCTGGGGACAGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTT  
 CAGGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACAGGCCAGCCCTACACCAATCA  
 CGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC  
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA  
 TCGAACCTATCGGGCCCTGATAAGCGGGTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTACCCAGCTGCGGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG  
 CCGGGGCGGGTGCCCGAGGGCGAGGAGGCTGCGGGGAGGCCCATACACCCAGCCGTCCA  
 CTCCAACCAAGCCCCAGTACCCAGGCCCGCGAGGGCAACCTGCCGTCTCTATTGCGCCCG  
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGG  
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT  
 GGAAGTGGAGGGAGTGAAGGTCCCTTGGAGCCAGGCCGAAGGCCACAGAGGGCGGTGGAG  
 AGGCCCTGCCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCCTC  
 CAGTACCCCTCCACGCAAGGCCCTACATCT**TAAG**CCAGAGAGAGACAGGGCAGCTGGGGCGG  
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCC  
 CAACCTCGGGATGTGTGCGAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTCCCTCTGGA  
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCAGAAC  
 CGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG  
 GGCCCTGCCATGTGCTGGTAACGCATGCCGTGGGTCTGTGGGCTCTCCCACTCCAGCGGA  
 CCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGCGGCTGTG  
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA  
 GGAACATGTTTTTGTCTTTTAAAAATATATATTTATAAGAGATCCTTTCCATTTATTCTG  
 GGAAGATGTTTTTCAAACCTACAGACAAGGACTTTGGTTTGTAGACACAACGATGATATG  
 AAGGCCTTTGTGAAGAAAAATAAAGATGAAGTGTGAA

**FIGURE 32**

MCSRVP LLLPL LLL L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N  
G I T M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R  
R L E R L Y L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E I R A L P P L R L P R L L L L D L S H N S L L A L E P  
G I L D T A N V E A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G  
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G  
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S  
S S L A P T W L S P T A P A T E A P S E P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E  
G F T G L Y C E S Q M G Q G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L  
T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A  
V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G  
P L E L E G V K V P L E P G F K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I



**FIGURE 33**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT  
 CTTTCATCATTTCATATGAGAAATTAAGTGGTAAATCCTTGGAAATFACA**ATG**AGACTCATCAG  
 AAACATTTACATATTTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG  
 AAGAAAGGGGACCTGATGACCAACTGCTCCAAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG  
 ACCCCAGCCACAAACGACACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA  
 TTTTCATCTGTCTCCAACCTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGG  
 ATCTCAAAACCTTTGAATTCACAAGGAGTTAAGATATTTAGATTGTCTAATAACAGACTG  
 AAGAGTGTAACTTGGTATTACATGGCAGGTCTCAGGTATTTAGACTCTTTCTTTAATGACTT  
 TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGA  
 GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATCTGTC  
 TTCTTAGGATTGAGAACCTCTTCTCATATTGAAGAAGGTAGCCTGCCCATCTTAAACACAAAC  
 AAAACTGCACATTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTGCGGTGATGGAATCA  
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA  
 ATGCAACGAAATCTTAGTTTAGAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA  
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTGGCATACATCAGTGGAAACAT  
 TTCAGATCCGAAATGTGACTTTTTGGTGGTAAGGCTTATCTTGACCACAATCTATTGACTAC  
 TCAAATCTGTAATGAGAACTATAAAATGGAGCATGTACATTTAGAGTGTTTTACATTGCTAC  
 ACAGGATAAAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGCAATATCTAAATG  
 CACAAATGGCACACATGCTTTTCCGGAATTTCTACGAAATTTCAATATTTAAATTTTGGC  
 AATAATATCTTAAACAGACGAGTTGTTTAAAGAAGTATCCAACCTGCCTCACTTGAAGAACTCT  
 CATTTTGAATGGCAATAAAGCTGGAGACACTTTCTTAGTAAGTTGCTTTGCTAACCAACACAC  
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAAAATGATGAAAATTTGCTCA  
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCAACAAATAAATGTCTGATTCTGCTTTCAG  
 GTGCTTGCCCAAAAGTATTAATACTTACCTAAATAAATAACCAAACTCAAACTGACTACCTA  
 AAGAGACTATTTCATCTGATGGCCTTACGAGAATAAATATGCAATTTAAATTTTCTAAGTGT  
 CTCCCTGGATGCACTCATTTCAGTAGACTTTTCACTTCTGAACATTGAAATGAACCTCATTCT  
 CAGCCCATCTCTGGATTTTGTCTCAGAGCTGCCAGGAAGTTAAAACTCTAAATGCGGGGAAGAA  
 ATCCATTCCGGTGTACCTGTGAATTAATAAATTTTCACTCAGCTTGAAACATATTACAGAGGT  
 ATGATGGTTGGATGGTCAGATTATACACCTGTGAATACCTTTTAAACCTAAGGGGAACATAG  
 GTTAAAGACGTTTCATCTCCACGAATTAATCTTGCAACACAGCTCTGTTGATTGTCCACCATG  
 TGGTTATTTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC  
 TGGTATCTCAGGATGCTAGGTCATGCACACAAACATGGCACAGGGTTAGGAAAACAACCCA  
 AGAACCACTCAAGAGAAATGTCGGATTCACGCATTTATTTTCATACAGTGAACATGATTCTC  
 TGTGGGTGAAGAAATGAATTGATCCCAATCTAGAGAAGGAAGTGGTTCTATCTTGATTGCTG  
 CTTTATGAAAGCTACTTTGACCTTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA  
 GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCACTTTGTCCAGAAATGAGTGGTGCCATT  
 ATGAATCTACTTTTCCACACCAATCTCTCCATGAAAATTTGATCATATAATTTCTTATC  
 TTACTGGAACCCATTCCATTCTATTGCATTTCCACCAGGTATCATAAACTGAAAGCTCTCCT  
 GGAAAAAAGACATACTTGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCAA  
 ACCCTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAATGCGAGACA  
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACACAGATTGCT  
**ATAAAAT**CCCAAGCTCCTTGGGAAGTTGGGGACCAATACACTGTTGGGATGTACATTGTATA  
 CAACCTTTATGATGGCAATTTGACAAATTTATTAATAAATAAATGGTTATTCCTTCTATA  
 TCAGTTTCTAGAAGATTTCTAAGAATGTATCCTATAGAAACACCTTCACAAGTTTATAAGG  
 GCTATTGGAAAAGGTTGTTACATCCAGGATTGTTTATAATCATGAAAATGTGGCCAGGTTGC  
 AGTGGCTCACTCTGTAACTCCAGCACATTTGGGAGGCCAAGTGGGTGACCCACGAGGTCAA  
 GAGATGGAGACATCCTGGCCAAACATGGTGAACCCCTGTCTCTATAAATAACAAAAATTA  
 GCTGGGCGTGATGGTGCCACGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGAGAAATCG  
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCCTGGT  
 GACAGCGCAGACTCCTATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAATGAAAAACATCC  
 TCATGGCCCAAAAAATAAGGTCTAATTCATAAATATAGTACATTAATGTAATATAATATTA  
 CATGCCATAAAGAAATAAGGTAGCTGTATATTTCTGGTATGGAAAAACATATTAAT  
 GTTATAAATCTATTAGGTTGGTGCAAACTAATGTGGTTTTTGGCCATTGAAATGGCATTGAA  
 ATAAAGGTGTAAGAAATCTATACAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTTGGA  
 TTACAGGGAGCATTTGATTTCTATGTTGTGTATTTCTATATGTTTGAATGTTTGAATGA  
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT



**FIGURE 35**

GGGGGCTTTCTTGGGCTTGGCTGCTTGAACACCTGCCTCCAAGGACGGGCTCGGAGGGGTTCGGCGGGAAAGG  
 GAGGAGAAGGAAGGCGGGGCGGGCCCTTCGCGCCGCGCCGCTCTGCGCGCCCTGTCCGCGCCGCGC  
 CAGCCCGAGCCAGCCCGCGGGCGGTCACACGCGCAGCCAGCCGCGCTCCCGCGCCCAAGCGCGCCGCT  
 CTGCTGTGCTGCTCGCCCTTGCCTCGCGCCAGCTTCTGCGCCCGCAGCCCGCGCGCCCGCGTGAACCGTGA  
 CCCTGCCCTGGGCGCGGGGCGGAGCAGG**CATG**TCCCGCCCGGGGACCGTACCCAGCGCTGGCCCTGGTGCCT  
 CTGGCAGTGAACCTTGGCGGGGTTCGAGGCCAGGGGCGAGCCCTCGAGGACCTGATTATTCGGGACGAGAGAT  
 CTGGAGCGGAGCCCTACTACGCGCGCCCGGAGCCGAGCTCGAGACCTCTCTCCGCGCTGCTCGCGGGG  
 CCGGGGAGGAGTGGGAGCGCGCCCGCAGGAGCCAGGCCGCCCAAGAGGGCCACCAGCCCAAGAAAGCTCCC  
 AAGAGGGAGAAGTGGCTTCGGGAGCCGCTCCACAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAG  
 CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCGTGAAGATGTGAGAGAGAGTTGCCACCTC  
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTGGGGGCA  
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTTATACGGAGCGCTGTGCGCGGGAAG  
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCTGACCAGATTCACTGGTGTATCACTCAAGGGA  
 GGAACCTCCCTCGGCTGAGTGACTGGGTGACATCCTATAAGGTCATGGTGAAGCAATGACAGCCACAGTGGGTG  
 ACTTTAAGAATGGATGTGAGACATGATATTTGAGGAAACAGTGAAGAGGATCCCTGTTCTCAATGAGCT  
 ACCGTGCCCATGGTGGCCCGCTACATCCGCAATAAACCTCAGTCTGTGGTTTGATAATGGGAGCATGTGCATGA  
 GATGGAGAGTCTGGGCTGCCCATGCCAGATCTTAATAATTATTAATCACCGCCGGAACGAGATGACCACCAT  
 GATGACCTGGATTTAAGCACCAATATAAGGAAATGCGCCAGTTGATGAAGTTGTGAATGAATGTGTCTCC  
 CAATATCCACGAATTTACAACATTTGGAAGAACGCCACGAGGCTGAAGCTGTATGCTGGAGATCTCAGATC  
 ACCCTGGGAGCATGAAGTGGTGAGCCGAGTTCACCTACATCGCGGGGGGCCACGGCAATGAGGTGCTGGGC  
 CGGGAGCTGCTGCTGCTGCTGGTGAGTTCGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATGTCCACCT  
 GGTGGAGAGAGCGCGGATTACGCTCCTCCCTCCCTCAACCCGATGGCTACGAGGAAGGCTACGAGAGGGGCT  
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATGACATCAACCAACACTTTCCTGATTTA  
 AACACGCTGCTCTGGGAGGACAGGATCGACAGAATGTCCGAGGAAGTCCCAATCACTATTGCAATCCC  
 TGAGTGGTTTCTGTGCGAAAATGCCAGGTGGCTGCCAGAGCCAGAGCAGTCAAGCTGGATGGAATAATCC  
 CTTTTGTGCTGGGCGGCAACCTCGAGGGCGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGGTCCCC  
 TGGAAAGACGAGGAACACACCCCCACCCCGATGACCAGTGTTCGCTGGCTGGCCCTACTCCTATGCTCCAC  
 ACACCGCTCATGACAGACGCCCGGAGGAGGCTGTGCCACAGGAGGACTTCCAAGAGGAGGAGGCACTGTCA  
 ATGGGGCTCCTGGCACACCGTCTGCTGGAAGTCTGAACGATTTCACTACCTTCATACAACTGCTTCGAAGT  
 TCCATCTAGTGGGCTGTGATAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGAGAATAACCGGGAATC  
 TCTGATCGTGTTCATGGAGCAGGTTCACTGTGGCATTAAAGGCTTGTGAGAGATTCACTGGAAGGAATCC  
 CAAACGCCATTATCTCCGTAGAAGGCATTAAACATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCTC  
 CTGAACCTCGAGAGTATGTGGTCACAGCAAGGCCGAAGGTTTCACTGCATCCACCAGAACTGTATGGTTGG  
 CTATGACATGGGGGCCACAAGGTGTGACTTCACACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGG  
 AGAAGTTTGGGAAGCAGCCCGTCAAGCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACGCT  
 GGG**TGA**CCCTCCTGGGCCCTTGAGACTCGTCTGGGACCATGCAAAATTAAGCAACCTGGTAGTACCTCCATAG  
 TGGACTCACTCACTGTTGTTCCCTGTGAATTCAGAAGTGCCTGGAAGAGAGGTTGATTGTGAGGCAGGTCC  
 CAAAAGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTCTTTGTTCCATTTATCCAAATAACTTGGACAGGCA  
 CGAGAGAAAACCTGATGGAGTGAGAGAATCAGCAAGCCAACTGGGAATCAGAGAGAGAGGAGAGAGGAGG  
 GAGCCTGTCCGTTTCAGAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGCTTCCCTGTTTGCCTGGCAGCAAGG  
 GTTCACGTGCAATTTGCAATTTGACAGCTAAAATTCAGCAGTTTCCCGAGTGGGCTGTGCCAAATGTTACCA  
 TTTGAGATGCTCCAGGCGTCTAAGAGAATCCACCTCTCTGGCCCTGGGACATGCAAGCTGCTACAAATAA  
 ATTCTGTGTTCTTTGACATAGCGTCAATTGCCAAGTGCACATCACTGAGCTCTTTGACTCTGTTTGAATCTCT  
 TTTTCAACAAGGAGTGTGTTCAAGAAAGAGAGAGAGGCTGAGATCACTCAGGAGTTTGTGGCAGCAAGCA  
 TGGAGCTCTTGCACAATTTCTGGGTCATAAACAACCCCAAGTCCCTGCTGATCCAGTAGCCCTGGAGTT  
 CCCAGGTAGGAGAGCCAGAGGTGCGAGCCTTCCGTAAGGGCCAGAGAAAATTAGCCTGGATCTCCTCTTTAC  
 CTGCTAGGACTGGAAGAGCCAGAAGTGGGTGGCTGAAGCCCTCTCTCTGCTGAGGTATGCCCTGTGTG  
 GAATGAGTGTCTCATGGGTGGCCCTCATATCAGCCTGGGAGTTATTTTGATATGATGCAAGTCTCTCCA  
 GATTAGGCTAAATGAATGAAAACCTCTTAGGATTATCTGTGGAGCATCAGTTTGGGAGGATTAATGAATTA  
 CTTGCAAGAAAAAGTATGTCTCACTTTTTGTTAATGTTGCTGCCTCATTGACCTGGGAAAAATGAAAAAAA  
 AATAAGCAAAATGGTAAGACCTTAAAAAAGGAG

**FIGURE 36**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPPDYQGQEIWSREPPYARPEPELETFSPLP  
AGPGEWERRPQEPRPPKRATKPKKAPKREKSAPEFPPPGKHSNKKVMRTKSSEKAANDHS  
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGLNIQAGINENDFYDGAWCA  
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNSHTWVTVKNGSGDMIF  
EGNSEKEIPVLNELPVPMPVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT  
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPVSLNPDGYEKAYEGG  
SELGGWSLGRWTHDGDIDINNFPDLNTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAA  
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYST  
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES  
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPTNAIISVEGINHDIRTANDGDYWRL  
NPGEYVVTAKEGFTASTKNCMVGYDMGATRCDFTLTKTNMARIREIMEKFGKQPVSLPARR  
LKLGRGRRRQRG

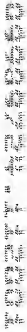
**FIGURE 37**

CTAAGAGGACAAG**ATG**AGGGCCCGGCTCTCATTTCTCCTAGCCCTTCTGTTCTTCCTTGGCCAAAGCTGCAGGGG  
 ATTTGGGGGATCTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTTCCCAAGTGTGACTCCAGCTCCAGC  
 TTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGACGCTTAGGCAGCGGAGGTTCTGTGTCCAGTTGTT  
 TTCCAATTTCACCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGTCTGTTCCTGCCAGACACCACCTTTC  
 CCGTGGACAGAGTGGAAACGCTTGGAAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAAGACTTTCTAAA  
 GTGAGGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAAACTGTTAAACCTAACTGTCCGAATTGACATCAT  
 GGAGAAGGATACCATTTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGA AAAAC  
 TGGTCATACAGCTGAAGGAGAGTTTTGGTGGAACTCAGAAATGTTGACCAGCTGGAGGTGGAGATAAGAAAT  
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAACAAATGTCCTGGCATTCCGCCAGAAATCGTGGC  
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAAACACCCCTGTCGTCCACCTCTCTCCACT  
 CAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAAACCGCTCTGTGGTTCAGCTCAACTGGAGAGGGTTT  
 TCTTATCTATATGGTGTGGGGTAGGGATTACTCTCCCAGCATCCAACAAAGGACTGTATTGGTGGCGCC  
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA  
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGTAGTGGTACAGCAGTTTACAACAACACATGTACGTCAAC  
 ATGTACAACACCGGAATATTGCCAGAGTTAACTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA  
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG  
 GATTGTGGGTTATTTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT  
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTTCATGGTATGTGGGGTTCT  
 GTATGCCACCGTACTATGAACACCAGAACAGAAGAGATTTTTTACTATTATGACACAACACAGGGAAGAGG  
 GCAAACCTAGACATTGTAAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCTTTTGACCAGAAA  
 CTTTATGTCTATAACATGGTTACCTTCTGAATTATGATCTTTCTGTCTTGAGAAGCCCCAG**TAA**AGCTGTTTA  
 GGAGTTAGGGTGAAAAGAGAAAATGTTTGTGAAAAAATAGTCTTCCACTTACTTAGATATCTGCAGGGGTGT  
 CTAAAAGTGTGTTCAATTTTGACGAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT  
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCCTTTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGA  
 TTGTCAAGGCTTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACATAGAAGCCTTAAATTA  
 GGAATTAAGGAACCTAAACCTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC  
 CTCATCCATGTAGCACCACTAATTTCTTCATGCGCTGGAAGAAAACCTGGGGACTTAGTTAGGTAGATTAATATCT  
 GGAGCTCCTCGAGGGACCAAAATCTCCAACCTTTTTTTCCCTCACTAGCACCTGGAAATGATGCTTTGTATGTGG  
 CAGATAAGTAATTTGGCATGCTTATATATTCTACATCTGTAAGTGCTGAGTTTATGGAGAGAGGCCCTTTTT  
 ATGCATTAATTTGTACATGGCAAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTCTTTTCTCTC  
 ATTGTCCACCTTACTAAAGTCACTAGAATCTTCTACCTCATAACTTCCTTCCAAGGCAGCTCAGAAGATTAG  
 AACCAGACTTACTAACCAATCCACCCCCACCAACCCCTTCTACTGCCTACTTTAAAAAAATTAATAGTTTT  
 CTATGGAAGTATCTAAGATTAGAAAAATTAATTTCTTTAATTTCAATTATGGACTTTTATTACATGACTCTA  
 AGACTATAAGAAAATCTGATGGCAGTGACAAAGTGCTAGCATTTATTGTTATCTAATAAAGACCTTGGAGCATA  
 TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTTTGCCTTTGTTTAAAGCCTGGAACCTGTAAGAAAA  
 GAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT  
 TGGAACTTGTCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT  
 TCGTTTTCATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTTACTCCCCCTTTTAAAAATAATGAT  
 TAAAAATGCTTTGAAAAA AAAAAAAAAAAAAAAAAA

1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
 0

**FIGURE 38**

MRPGLSFLALLFFLGLQAAGDLGDVGPPIPSPGFSSFPGVDSSSSSFSSSSSRGSSSSSRSLGS  
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV  
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ  
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTFVVHPPPTPGSCGH  
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRYLYNTLD  
DLLLYINARELRITYGQGSCTAVYNNNMVNMVNTGNIARVNLTNTIAVTQTLPNAAAYNNR  
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF  
MVCGLVLYATRTMNTTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFQKLYVYNDG  
YLLNYDLSVLQKPQ





**FIGURE 40**

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT  
 CCGCTGCTCTTGTGACGTTGTGGAG**ATG**GGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCT  
 GGAATACCATGTTTTGTGGAAAGTGCCCCGTGTTTGTCTGCGGATGCTGTCTAGTGGAAAC  
 AACTCCACTGTAACTAGATTGATCTATGCACTTTTCTTGCTTGGTGGAGTATGTGTAGCTTG  
 TGTAAATGTTGATACACGGAATGGAGAACAACATGAATAAGATTCCCTGGATTTTGTGAGAATG  
 AGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAAGCTGTATATCGTTTGTGCTTT  
 GGTTTGGCTATGTTCTATCTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA  
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCGAGCAATTGCAATTA  
 TTATTGGGCGAGTTCTTCAATCCAGAGGAACCTTTTACAACGTGTGTGGTTTTTGTAGGCATG  
 GCAGGTGCCCTTTTGTTCCTCCTACATACTAGTCTTACTTATTGATTTTGCACATTCATG  
 GAATGAATCGTGGGTGAAAAAATGGAAGAGGGAACTCGAGATGTTGGTATGCAGGCTTGT  
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTCTGTTCTTTGTCTAC  
 TACACTCATCCAGCCAGTTGTTCCAGAAAAACAAGGCGTTTCACTAGTGTCAACATGCTCCTCTG  
 CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAAGATCACAACCAAGATCTGGTT  
 TGTTACAGTCTTTCAGTAATTACAGCTACACAATGTATTTGACATGCTCAGTGTAGACCAAT  
 GAACCAAGAAACAAATGCAACCCAGTCTACTAAGCATAAATGGCTACATACAACCAAGCAC  
 TGTCCCAAGGAAGGGCAGTCACTCCAGTGTGGCATGCTCAAGGAATTATAGGACTAATTC  
 TCTTTTTGTGTGTATTTTATCCAGCATCCGTACTTCAAAACAATAGTCAGGTTAATAAA  
 CTGACTCTAACAAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATC  
 ACTGGAGGATGGGGACGATGTTCCAGCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA  
 GTTATTCCCTTCTTTCACCTTCATGCTTTTCCCTGGCTTCACTTTATATCATGATGACCTTACC  
 AACTGGTCCAGGATGAACCCCTCTCGTGAGATGAAAAGTCACTGGACAGCTGTCTGGGTGAA  
 AATCTCTCCAGTTGGATTGGCATCGTGTGTATGTTTGGACACTCTGGCACCACCTTGTCT  
 TTACAAATCGTGATTTTGAC**TC**AGTGAGACTTCTAGCATGAAAGTCCCACTTTGATTATTGC  
 TTATTTGAAAACAGTATCCCAACTTTTGTAAAGTTGTGTATGTTTTTGGCTTCCCATGTAAC  
 TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTTTCTTACCAA  
 GTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTATGAATATGGTGTAGT  
 TAGTAAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA  
 ACAAATTTTGTGACTATTTTAAATATATATAGACCTTAAAGCTGTTTTAGCAAGCATTAAA  
 GCAAATGTATGGCTGCCTTTTGAATATTTGATGTGTGCTGGCAGGATACTGCAAAGAAC  
 ATGTTTTATTTTAAATTTTATAAACAAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA  
 AGGTTTTACCTTGTATACGGAATTTACACAGGTAGGAGTGTTTGTGGACAATAGTGTAGG  
 TTATGGATGGAGGTGTCCGTACTAATTAAGTAACGAGTAAATAATCTTACTTTGGGTAGAGA  
 TGGCTTTGCCAACAAAGTGAACCTGTTTTGTTGTTTAACTATGAAGTATGGGTTCACT  
 GGAAATGTTTGGAACTCTGAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA  
 AGGAAGTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCCCAGCAGGTAGCTCAGCCTT  
 GGTAAATCCGACACTTTGGGAGCTTAAGTGGGTAGATTACTTGAGCCCAAGGAATTACAGACA  
 GCTTGGCAGATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCCCTGTGGTC  
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCCAGAGCCAAAGGTTGCAGTGAGCAAGTCA  
 CGTCACTGCCTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATTGAAATCAAGG  
 AGGCAAAAATTTGACAGGGAAGGAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTTAT  
 ATAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA  
 GCTCAGATAGCTAATTAGGAATTTCAAGTTGGCCAATAATAGCATCTCTCTGCATTTAA  
 AATAAATTTCTATTCAAATATACATCATATTGATTATACACCTCATACTGTGATAATTAATGT  
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAACAGGTGAGAAGATGATGGAATGTTTTT  
 AGAATAAAGTCTGCTTATAGTATACACAGTTCAAAGATGTTTTAAATGCTTTTGTAT  
 TTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGT  
 ATGAGAGTTTGTATTGTTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTCAAT  
 TCTTCTTTAAAAATTTTATTAATGTAATGGAATATAACAAATTCAGCTTAATCCCCAAC  
 TTATTCTGTGTGAGACATTGTATTCCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA  
 ATGAATTCAGAGAAAAA

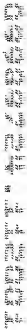






**FIGURE 43**

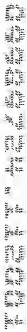
GTTATTGTGAAC TTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAACAANTCC  
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATACCAGGAATGGAAGAACAAC TGAATAAGATT CCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG  
GGGC



AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATAACCATGTTTGTGTGGAAGTGCCCCGTGT  
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCACTGTAACTAGATTGATCTATGCACTT  
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC  
GAATAAGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTG  
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA  
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT  
CTTTAAATTGTCTGCAGCAATTGCAATTATTATTGGGGC

**FIGURE 45**

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACTTTTTCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACACTGAATA  
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTGTAAACATTTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT  
ACAACTGTGTGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT  
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC  
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG



**FIGURE 46**

CTCGGGCGCGCACAGGCGAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGGCGCGGCCCTCTCCAAT  
GGCAATATGTGTGGCTGGAGGCGAGCGGAGGCTTCGGCAAAGGCAGTCGAGTGTTTGCAGACCGGGGCGAG  
TCCTGTGAAGACGAGATAAAAGAAAAACATTTATTAACGTGTCATTACGAGGGGAGCGCCCGCGGGGCTGTGCG  
ACTCCCCCGGAAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGCGGAAAGAGGCGAGATTAC  
TCGTGTTCCAGCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATATGCGATGCG  
CCCTGTTTGTGTATTACGCACACACAGCTGCACACAAGGCTCTGGCTCGCTCCCTCCCTCGTTTCCAGCTCC  
TGGGCGAATCCACATCTGTTTCAACTCTCCGCCGAGGCGAGCAGGAGCGAGAGTGTGTGCAATCTCGGAGTG  
AAGAGGGACGAGGGAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAAGCACCAGAT  
CAGCAAAAAAAGAAGATGGGGCCCCCGAGCCTCGTGCTGTGCTTGCTGTGCCCACTGTGTCTCCCTGTCTGGG  
TGAAGCTCGGCCCTTCCTGTGCGACCAACCGCTTGAAGGCAAGGTTTCAGAGGGACCGCAGGAACATCCGCCCA  
ACATCATCCTGGTGCTGACGGACGACGAGGATGTGGAGCTGGGTTCCATGCAAGGTGATGAACAAGACCCGCGC  
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCCCTTCGTGACCACCCATGTGCTGCCCTCACGCTCCTC  
CATCCTCACTGGCAAGTACGTCCACAACCAACAACACCTACACCAACAATGAGAATGCTCCTCGCCCTCCTGGC  
AGGCACAGCAGCAGACCGCACCTTTGCGGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG  
TATCTTAATGAATGACACCGCTCTTACGTGCCACCGGCTGGAAGAGATGGGTCCGCTCCTTAAAAACTCCG  
CTTTTATAACTACACGCTGTGTGCGGAACGGGGTGAAGAAGAAGCAGGCTCCGACTACTCCAAGGATTACCTCA  
CAGACTCATACCAATCGACAGCTGAGCTTCTTCGCGACGTCGAAGAGATGTACCCGACAGGCGATCCTC  
ATGGTCACTCAGCCATGCAAGCCCCACGGCCCTGAGGATTACGCCCCACAATATTCACGCTCTTCCCAAGCCG  
ATCTCAGCACTACGCGGAGCTACGCACTACGCGCCCAACCCGGACAACACTGGATCATGCGCTACACGCGGG  
CCATGAAGCCCATCCCATGGAATTACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCCTCATGTGCGTGGAC  
GACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGC  
CGAACACGGTTACCAATCGGCCAGTTTGGCCTGGTGAAGGGGAATCCATGCCATATGAGTTTGCATCAGGG  
TCCGCTTCTACGTGAGGGGCCCCAACGTTGAAGCGCGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTG  
GCCCCACCATCCTGGACATTCGAGGCTTGACATACCTGCGGATATGGACGGGAATCCATCCTCAAGCTGCT  
GGACACGAGCGGCGGTGTAATCGGTTTCACTTGAAGAAGAAGATGAGGCTTGCAGCGGACTCCTTCTTGTGTG  
AGAGAGGCAAGCTGCTACACAGAGAGCAATGACAGGTGGACGCCGAGGAGGAGAATTTCTGCCAAGTAC  
CAGCGTGTGAAGGACCTGTGTGACGCTGCTGAGTACCAAGCGGCTGAGCAGCTGGGACGGGACAGAAGTGGCAGT  
TGTGGAGACGCCACGGGGAAGCTGAAGCTGCATAAGTGAAGGGGCCATGCGGCTGGGCGGCGAGCAGACCCC  
TCTCCAAGCTCGTGCCCAAGTACTACGGGACGGGACGCGAGGCTGCACCTGTGACAGCGGGACATCAAGCTC  
AGCCTGGCGGACGCCGGAAGAACTCTCAAGGAAGAAGTACAAGGCGAGTATGCGCGAGCTCGCTCCATCCG  
CTCAGTGGCCATCAGGTTGGACGCGGAGGTGTACCAGCTAGGCTGGGTGATGTCGCCCGGACCCGGAACCTCA  
CCAAGCGCACTGGCCAGGGGCCCTGAGGACCAAGATGACAAAGATGGTGGGGACTTCAGTGGCACTGGAGGC  
CTTCCCGACTACTCAGCGGCCAACCCCATTAAGTGACACATCGGTGCTACATCCTAGAGAACGACAGTCCA  
GTGTGACCTGGACCTGTACAAGTCCCTGCAAGGCTTGAAGAGCCACAAGCTGCACATCGACACCGAGATTGAAA  
CCCTGCAAGACAAATTAAGAACCTGAGGGAAGTCCGAGGTCACCTGAAGAAAAAGCGGCGAGAGAATGTGAC  
TGTCACAAAATCAGCTACCACACCCAGCACAAAGGCCGCTCAAGCAGAGGCTCCAGTCTGCATCCTTTGAG  
GAAGGCGCTGCAAGGAAGGACAGGTTGGCTGTGTCGGGAGCAGAAGCGCAAGGAAGAACTCCGCAAGCTGC  
TCAAGGCTCGCAGAACACGACACCTGACGATGCCAGGCTCACGTCCTACCCACGACAACGACACTGG  
CAGACGGCGCTTTCTGGACACTGGGGCTTTCTGTGCTGCCACAGCGCCCAACAATAACACGTACTGGGTGAT  
GAGGACCATCAATGAGACTCACAAATTCCTCTTCTGTGAATTTGCAACTGGCTTCTTAGAGTACTTTGATCTCA  
ACACAGCCCCATCAGCTGATGAATTCAGTGAACACACTGGACAGGGATGCTCTCAACCGCTACACGTACAG  
CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGACCTGATGAGG  
AAGCTATGACCAATACAGGCACTTCAGCTCGAAAGTGGCCAGAATTAAGAGCACTTCTTCAACATCACTGG  
GACAACTGTGGGAAGGCTGGGAAGTTTAAAGAAACAACAGAGTGGACCTCCAAAAACATAGAGGCATCACCTGA  
CTGCACAGGCATGAAGAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCTCGAGAAGC  
AAGACGCACTCTCAGTCACATGACAGATTCTGGAGGATAACCAAGGAGCAGAGGATCACTCAGGAAGTCC  
ATTTTGGCCCTGCTTTGCTTTGGATTATACCTCACCAGCTGCACAAATGCAATTTTTCGTATCAAAAAGT  
ACCACTAACCTCCCGACAGGCTCACAAAGGAAACGGAGAGAGGACGAGGAGAGATTTCCTTGGAAATTC  
TCCCAAGGGCGAAAGTCATTGGAATTTTAAATCATAGGGGAAAAGCAGTCTGTTCTAAATCCTCTTATCTT  
TTGGTTTGTGCAAAAGAAGAACTAAGAAAGCAGGACAGGCAACGCTGGAGAGGCTGAAACAGCTGCAGAGAC  
TTTGACAAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTATAAACCCCTGGTTGCTCTGAAGAA  
CTGCCCTCATGTATATATGTGACTATTTACATGTAAATCAACATGGGAACCTTTTAGGGGAACCTAATAAGAAAT  
CCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAGAAAAA

**FIGURE 47**

MGP PSLVLC LLSATV FSL LGSSA FL SHHRLKGR FQRDRRNIRPN IILVLTDDQDVELGSMQ  
 VMNKTRRIMEQGGAHFINAFVTTPMC C PSRSSILT GKYVHNHNTYTNNENCSSPSWQAQHES  
 RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
 YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP  
 SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT  
 YIVYTADHGYHIGQFGLVKGKSMPIEFDIRVPFYVRGPVNEAGCLNPHIVLNIDLAPTILDI  
 AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVD AQEEN  
 FL PKYQ RVKDL CQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY  
 YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAAQ  
 PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDL DLYKS  
 LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHRGSSL  
 HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCTHDNQHWQTAPFWTLG  
 PFCACTSANNNTYWCRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
 HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRFPSSKSLGQLWEGWEG

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**FIGURE 48**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAC**CATG**CTGGGCCTCCTGGGGAGCACAGCCC  
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGGCCACC  
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGAAAA  
CCGAGTCCGCCGGGCCCCAGCCTTGGCCCTTCCGGCGGGGGGCCACCTGGGAATCTTTCACC  
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
CCCCGCCACACCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
CGCTCGC**TGA**GGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG  
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG  
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTCATGGCATGCCCCAGTGTACTATGGC  
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTTGGGGAGTGGAGAGCAAGG  
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG  
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
ATCAGGCTGCTGCAGGCCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT  
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAT  
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA





**FIGURE 50**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA  
CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG  
GTACTCAGGGCTACTGGCTGGGGTGGAAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA  
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGGCGCTTTTCACTGAGAGC  
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
CATGTGGTGACAGCCACCTTCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG  
TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATATCCTCGGCTGG  
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT  
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA  
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC  
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGAT  
GACGGTGACACCCCGAGCGAGCACAGCTACAGCGAGTCAAGTGCCAGCGGCTCCTCTTTTGA  
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC  
CCCTGGGACTACCAAGTGCTCTGGGAGCCACTGCCCTTGAGAAAGGGCAAGGAG**TAA**CCC  
ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAAGTGAAGCAGACTCTCCAGCAGACTCT  
CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCTTGC  
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA  
GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC  
ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA  
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**FIGURE 51**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR  
LFTESCISISPKLRSIAVYYDNPHMVPPDKCRCVGSILSEGEESPSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATRVRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPALAR  
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR  
LFTESCISISPKLRSIAVYYDNPHMVPPDKCRCVGSILSEGEESPSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATRVRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPALAR  
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

**FIGURE 52**

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT  
GCCCCGCGCCAGTC**ATG**ACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT  
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA  
GACACGCTTCACATACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
GACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA  
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT  
GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT  
GATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG  
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAAT  
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**  
**A**TAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 53**

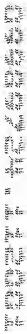
MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRRAIPSHLAYGKRGF  
PPSPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNKSKKK



CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC  
CCCGCGCCAGTCATGACCTTGGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTACATACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCTCTGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG  
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCCTGCTGAGGG  
ATGGCCATGTGCCACCCTCCTGGGCTCATTGGGTATACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAAGAACTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTTAAAAAATTA

**FIGURE 55**

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGTT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA



**FIGURE 56**

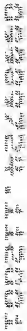
CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG  
TGAGGCGGGCGCGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG  
ACCTGAAAAAAATGCTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG  
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT  
TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT  
GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA  
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG  
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG  
CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT  
TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT  
TTCCACAGCACAAACAGCCCTGCATGGGTTTGTTTGTTTTTTTACTGCTCACTCCCAACCTT  
TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT  
AAAAATCAGGAGAACCTAAACAACAACCAAAATCTATTGTGGTATGCACTTGATTAACCT  
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT  
TGTA AAAAATAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA  
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT  
CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTTCCGTGG  
TCAAATTTCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATTTCTGTGAACATGTAAT  
GTA ACTGGCTTTTGAGGGTCTCCAAGGGGTGAGTGGACGTGTGGAAGAGAGAAGCACCAT  
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCATT  
CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC  
CACATCCACCACTG





**FIGURE 58**

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG  
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC  
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT  
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG  
CTCGCATTIGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT  
TTTCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC



**FIGURE 59**

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC  
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGGGCTTTT  
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT  
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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GGACACCGGGTTCGGACCAATGCANGACGGGGTGANTGACCTGAAAAAATGTTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT  
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATT  
CTGATTGNATTCTATGCGGATTCTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

TAGAGGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTNNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC  
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTTGGGTCAAACAGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAAATCGGGGGAGTGAGGCGGCCCGCGCGG  
CGNGACACCGGGTTCCGGGAACCATTCACGACGGGTGGACTGACCTGAAAAAATGTTTG  
GATTNTAGAGGCTTGAGATGCTCAGAAATGCATTGACTGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGTACTATTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGCTGCGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGCCCTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCTTGAATGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

**FIGURE 63**

CGACGCCGGCGT**CATG**TGGCTTCCGCTGGTGTCTCTCTGGCTGTGCTGCTGGCCGTCC  
TCTGCAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC  
AAACGGCCCCAGCGCCCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC  
TTTTTACGCCAACCAAGTGGCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG  
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGTGGAAACAACAT  
ACCAAGGCAGGGGGCTGCTGTCTACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAAT  
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTTGGCCGTTTTATCTTGGACCATCATG  
AAGGGCAGCTGGACTGGGCTCCCTGTCTCTCTCTTTTACATCATGGTACTGGAAGGGCCC  
AATGGCCGAAGGAGTACCCATGTACAGTGGAGAGAAAGCCTACATTACGGGCCCTCAAGGA  
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA  
GTGGAGCCCCCATGCCATCCTGTGAATTTCTCCCATTTGCCCGTGGTTCAGCTCCTCGAC  
AGGTGTGGGCTGCTGACTCGTTTTCTCTCCATTCCCTTCAAGCATCCACCCAGAGCCTGGCTGA  
GGTCTCTGCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA  
CTTACGGGTGTCAACCCCAACCAAGTGCCTTTTCCATGCAGCCCTGCTGGTCAACCACTAC  
ATGAAAGGGGCTTTTATCCCCGAGGGGTTCCAGTGAATTTGCCCTTCCACCATCCTCCTGT  
GATTACGCGGGCTGGGGGCTGCTCTCACAAAGCCACTGTGCAGAGTGTGTTGCTGGACT  
CAGCTGGGAAGCCTGTGGTGTCAAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC  
CCCATCTGGTCTCCAAGCAGGAGTGTCAACACCTATGAACACCTACTGCGGGGAACGC  
CCGCTGCCCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCGGCCCGGCTTAGGCATGACCT  
CTGTTTTTCATCTGCCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGTCCACCACTACTAT  
GTTTACTATGACACGGACATGGACAGGCAGTGGAGCGCTACGCTCTCATGGCCAGGGAAGA  
GGCTGCGGAACACATCCCTCTTCTCTTCTTCCATCAGCCAAAGATCCGACCTGGG  
AGGACCGATTCCAGGCGGGTCCACCATGATCATGCTCATACCCACTGCCACGAGTGGTTT  
GAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGCAGTGACTATGAGACTTCAAAAACCT  
CTTTGTGGAAGCCTCTATGTCAAGTGGTCTGAAACTGTTCCCAAGCTGGAGGGGAAGTGG  
AGAGTGTGACTGCAGGATCCCCACTCACCAACCAAGTCTATCTGGCTGCTCCCCAGGTGCC  
TGCTACGGGGCTGACCATGACCTGGGGCCGCTGCACCCCTTGTGTGATGGCTCCTTGAGGGC  
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTCACCTGTGGACTGGTCG  
GGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACTTGTACTCAGAC  
CTTAAGAATCTTGATTCTAGGATCCGGGACAGAAGAAAAAGAA**TAGT**TCCATCAGGGAGG  
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG  
CATTAGTTCTTGCAGGTATAAAGCACTCTAATTGGTCTGATGCCGTGAAGAGAGGCCCTAG  
TTTAAATCACAAATTCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA  
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGTATG  
TCTCATGACGAGCGGGCGCTCTGCTATCCCTCACCCTGCTCCTTAACCTAGTGTATCAAGCGA  
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGACGCTCAACCTGGTGGGTTCAGTTC  
TGTCCTGAGGCTTCTGCTCTCATTCAATTAGTGCTACGCTGCACAGTTTACACTGTCAAGG  
GAAAAGGGAGACTAATGAGGCTTAACTCAAACCTGGGGCGTGGTGGTGGTGGCATTCATA  
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCAGTGGCTCTTCAGGGGACAGGAAAT  
GGCTGTGTCTGGCCAGTGTGGTCTGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA  
GGGTGCATGTGAGATGATCATATCAATTATGGAAGTCCCGGGTCTGCTCTTCTTATCA  
TCGGGGTGGCAGCTGGTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC  
CTTATCCACCAATAACACAGGGAAGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGA  
TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCAGCCGAAGGG  
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTACATCAGAAAAAGGA  
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTCAGTTAATGACATGTGAGGG  
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTG  
GTATCAGACATCAAGAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATG  
ATTCCATTGCTTTAAAAA

**FIGURE 64**

MWLPLVLLLLAVLLLLAVLCKVYLGLFSGSSPNPFSEdVKRPPAPLVTDKEARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDGTGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ  
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTDMDQAMERYVSMPREEAAEH  
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNFSVEA  
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

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FIGURE 65

[illegible]

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTILTSDESVDHTTAGRVVAGQIFLD  
SESELESSIQEEEDSLKSQEGESVTEIDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG  
EPCHFPFLFLDKEYDECTSDGREDDRLWCATTYDYKADEKWGFCETEEAAKRRQMQEAEEM  
YQTGMKILNGSNKKSQKREAYRYLQKAASNHTKALERSVYALLFGDYLQNIIQAAREMFEK  
LTEEGSPKQQTALGLFYASGLGVNSQAKALVYYTFGALGGNLIAMHVLVSRL

**FIGURE 67**

CTTCCCAGCCCTGTGCCCCAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCTTGCCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTGG  
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT  
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT  
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG  
TTAATAATATTCAACATGTCAACAAC

CTTCCCAGCCCTGTGCCCCAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCTTGCCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTGG  
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT  
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT  
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG  
TTAATAATATTCAACATGTCAACAAC

**FIGURE 68**

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQGVAQLSCTLSPQHVTIRDYGVSWYQQRAG  
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTI SPVQPEDDADYYCSVGYGFS P

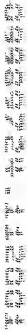
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**FIGURE 70**

MTPSPLLLLLLPPLLGAFFPAAAAARGPPKMADKVVPQRQVARLGRTVRLQCPVEGDPPLTM  
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGLSVNYTLVVLDDISPGK  
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIAFPVGSSVRLKCVASGHPRPDITWMK  
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL  
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD  
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA  
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS  
LAALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV  
HQHIHYQC



**FIGURE 71**

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAATCTCCAGGGGGACCCGATTCAGAGTCT  
 AGTGACTCTGTGAAGCACCCACATCTACCTCTTTGCCACGTTCCACAGGGGCTGGGGGAAAGATGGTGGGGGACCA  
 AGGCGTGGGTGTTCTCCCTTCCTGTCTCTGGAAGTCACATCTGTGTTGGGGAGACAGACGATGCTACCCAGTCGA  
 GTAAGAAGATCTCCAGCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCTGCCGACACCCCTGGAGAGCCGCTGG  
 TGAGTGGACCAACATGGTTCAACATCGACTACCCAGCGGGGAAAGGGGCGACTGATGAGCGGGTGGACGCCATTCGGT  
 TCTACTATGGGGACCGCTGATGTGTCGCTCCCTGCGGCTAGAGGCTCGGACCATGACTGGACACTGCGGGG  
 AGCATGGCCAGGTGGTCCATGGTAGTCCCCTGAGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCTGGGCCA  
 GAACTGCTCTAATTACACCGTAGCCTTCCTTGCCACCAGGATCCCTGGCCGAGACACAGAGCGCATGTGCGA  
 GCCCATGGTCTCCCTGGAGCAAGTGCTCAGCTGCCTGTGTTGACTGAGGCTGGGGTCCAGACTCGGCACACGATTTGC  
 TTGGCAGAGATGGTGTGCCTGTGCACTGAGGCGCAGCGAAGAGGGTCACTGATGGGCGAGGCTGTACAGC  
 CTGTGACCTGACCTGCCAATGGGCGCAGGTGAATGCTGACTGTGATGCCTGCATGTGCCAGAGCTTCATGCTTC  
 ATGGGGGCTGTCTCCCTTCCCGGAGGTGGCCAGCTCAGGGGCTGCTATCTACTCTCTGACCAAGACGCCGCTTC  
 CTGCTGACCCAGACAGACAGTGTATGGGAGATTCGAATCCCTGCTGTGCTGATGCTGCAAGAGCATCTCTGAA  
 GATCACAAAGGTCAAGTTTGGCCCATGTGTACTCAGATGTCGAAGTCTGAGGACAGCCACCATCAAGG  
 CAGAGTTTGTGAGGCAAGACTCCATACATGGTATGAACCTTGACACAAAGCACGAGAGCTGGGCAGAGC  
 GTGCTCTGTGCTGTGAAGGCCACAGGGAAGCCAGGCCAGACAAGTATTTTTGGTATCATAATGACACATTTGCT  
 GGATCCTTCCCTCTACAAGCATGAGAGCAAGCTGGTGTGAGGAAACTGCAGCAGCACACAGGCTGGGGAGTACT  
 TTTGCAAGGCGCAGAGTGATGCTGGGGCTGTGAAGTCCAAGTTGGCCAGCTGATTTGTCACAGCATCTGATGAG  
 ACTCTTGTCAACCCAGTTCCTTGAGAGCTATCTTATCCGGCTGCCCATGATGCTTTTCAAGATGCCAACATCT  
 CTCTCTACTATGACGTGGGACGCTGCCCTGTGTTAAGACTTTGTGACGGGCAGCAGGATTAATGGGATCAGGTGCGGTGT  
 ATGCTGTGCAGAACTGCTGTGGCATCTCTCAAGACAGAGGAAAGGAGGATCCAGTGCAGTGGCTACAGCTACCC  
 ACCAAGGTGGCCAAAGGATGCAGCTGCCAGCGGTGTACGGAACCTCGGAGCATCGTGGGGGGCCGTGTCAGTGG  
 TGCTGACAAATGGGGAGCCGATGGCGCTTTGGCCATGTGTACATGGGGAACAGCGCTGTGAAGCATGCTGCTGTACA  
 AGGGCACTTTTCACTCCCATGCTCCCCAGGACACTGAGAGGCTGGTGTCTCAGATTTGTGGCAAGCTGCAGAGAG  
 TTTGTCAACACCCAAAGTGCTACCTTTCAACAAGAAGGGGAGTGGCGGTTCCTCATGAATCAAGATGCTCTGTC  
 TCGGAAAGAGCCCATCACTTTTGAAGCCATGGAGAGCAACATCATCCCCTGGGGGAGTGTGTGTGTGAAGAC  
 CCATGGCTGAACCTGGAGATTCCTCCAGAGGTTTCTACAGGCAAGATGGGGAGCCCTACATACGAAGATGAG  
 GCCAGTGTGACCTCTCTGGATCCCGAATATTTCCAGAGCCAGATGCCAGCTGCCAGCTGACCTGACTTCATCA  
 TGACGAAGGAGACTCTTTCCCTCTTCCGACCTATGGCATGTTCTCTGTGACATCTCAGAGATGAGGTCACTTCAG  
 AGCCACTTAATGCTGGCAAGTGAAGTGCACCTTGACTCGACCCAGTCAAGATGCCAGAGCACATATCCACA  
 GTGAAACTCTGCTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAGGTGATTTCAAAATTTGAAAAATCAAG  
 GAGAAACAAAGAGAAGACAGAACCTTCTTGTGGGCAACCTGGAGATCTGTGAGAGAGGCTCTTTTAACTGG  
 ATGTTCTCTGAAAGAGGGGGTGTCTTTGTTAAGTGTAGGGGCTACCGGAGTGAAGGTCTTGTGCTTAGTGAGCAG  
 ATCCAGGGGGTTGTGATCTCCGTGATTAACTGGAGCTAGAAGTGGCTTCTTGTCCAACTTAGGGCTGGGG  
 CGGCTTTGACAGTGTCAACAGGCGCCAAAGCGGGGCTGTGTGCTGCCTTCTGTGATGACCACTCCCTGTGAT  
 CCTACTCTGCTTATGTCTTTGCAAGGCTGGCTGGGAGGAACTCGGACAGCTGGAGTCTTCTCTTAAATTCAC  
 CCAAATGCAATTTGGGCTCCCTCAGCCCTATCTCAACAAGCTCAACTACCGTCCGAGCGGACCATGAGGATCCAG  
 GTTTAAAGACAGCTCTTCCAGATTGAGCATGGCCAAAGCCAAAGCCCACTGAGTGAAGGAGCAATGGGCCCA  
 TCTATGCCCTTTGAGAACCTCCGGGCACTGTGAAGAGGCCACACCCAGTGCAGGCCACTTTCCGTTCTTACCAAGT  
 GAGGGGGATCGATATGACTTACAAACAGTCCCTTTACAGAGATGACCTATGAGCTGGAATGAGATATCTG  
 GGCATGGTGGCCAAAGCCGATGGAATTCAGGCGCTGCTATATCAGCTGATTTGGGGCACTGGAGATGATGA  
 ATCTGGGATCCGACATGGGGGCACTCATCGGCGCAAGTGGGGAAGCTGTATGGAATCCGAGATGTGAGG  
 AGCATCTGGGACAGGACACAGCCCATGTCTCAGCTGCCTGTCTGGAATTCAGTGCAGTGGGATGCTCTATGA  
 TCAGGACCTGTGGACCGCACCTGGTGAAGGTGATCCCCAGGGGAGTGGCGTGCAGCCAGTGTGAACCCCA  
 TGCTGCATGATGATGCTGTCAACCATTTGCCACTTGCACTCAACAACGACACCAAGTGAATACCAATGCTGGCA  
 CCCTTGGACCCACTGGGCCACAACATATGGCATCTACACTGTCACTGACCAAGGACCTCGCAGCGGCCAAGGAGAT  
 CGCGCTCGCGCGGTGCTTTGATGGCACATCGATGGCTCCTCCAGATATCATGAAGACAATGTGGGAGTGAAGCC  
 TCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCCTTTCAGTACCTCCAAAGACACCCAGCCGAC  
 TCCCTGTCTGCAGGCACTGTCCAAGGAAGTGCCTCGAGGAGGAGCAGGAGCGAGCGAGCGAGGCTGGCCAGCG  
 CAGGGTGGAGTGGTGGGCTCTCTGAGATTTCCTAGAGTTGTCTCAACAGCCCTCGATCAAC**TAA**GTGTTTTGTGT  
 ACTTCACTCCCTCTTCTGCGCTCATTTGATGTGACAGCCATTGTGAGACTGTGACACAACTGTGCTACTTGTGTAAT  
 TTAAGCACTTCTGTTTTGCGAATTTGCTGTTGTTGTTCTTCTGCTTACTTACTTTGTCCTGCTGCTACTGTA  
 TTGGCAGCTGGGCCCCCAATGGCAATTAAGCCCTTTGTGAACCTGTTCTTAAATCAACACAGAAAT  
 GGCCACTGGTAAATCTGTCAGCTTCACTTACTTATTAATGCCATTAATGCAATTAATCTCTCTCTGTT  
 TTTCCTGGTTTTGGCCACTCTGCATATGAGGAATCTGATCTGAGATCAAAATCAACATATAAACATAT  
 TTCTGGCTGTGCTCCACAGACATAGGCAAGCCTTGATCATAGTTACATACATATAAAGTGGTGAATAAAG  
 AAATAAAACACATACTTTTACTTGAATTAATAAATACTTATTTATTTCTTGTCTAAATTTGGAATTTAGTGG  
 ACATTAAGATTAAGCATTAATAATAGGGTGATCATAGTTCCCTACCAAGTGGTAAGAAAGACATCTCCCTGT  
 ATCCACAATTACACAGGTGTGTAAGTGTATTTGATCAATTTCCCTTTGCAATTCGCTTTTGTCTTGTCTGTAAGAA  
 CCAGTGTAGCCAGGCGAGTGTCAATAAGTATCACTCTGTATTTGCAAAAAA

**FIGURE 72**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPEGWTTWFNI  
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTDWTTPAGSTGQVVHGSPRGFWCLNREQ  
 RPGQNCNRYTVRFLCPPGSLRRDTERIWSWPSPWSKCSAACQGTGVQTRTRICLAEMVSLCS  
 EASEEGQHCMGQDCTACDLTCMPGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK  
 TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY  
 MVMNPETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG  
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFNATNSFYDVGRCPV  
 KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCCTETRSIVRGRV  
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFFVDRLQKFVNTTKVLPFN  
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV  
 KASVTFLDPRNISTATAAQTDLNFINDGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL  
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLNL  
 DVPESRRFCVKVRAYSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA  
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPR  
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFN  
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRVTGKLYGIRDVRS  
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAV  
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT  
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQRQASRGGRQGGVVASLRFPRVA  
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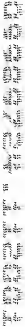


**FIGURE 73**

CTGCAAGTTGTTAAGCCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCTCAATATACCTGAATACGCAC  
 AATATCTTAACTCTTCATATTTGGTTTGGGATCTGCTTTGAGGTCACCTTTCACTTTAAAAAAAATACAGAG  
 ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGC  
 AAGCTCTGCTTTAGTTTCCAGAAGATTACAAAGAAATTTAGAGATGTTATTTGTCAAGATCCCTGTGCGATTGATG  
 CCGTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAAGACT  
 CAGATTTACACGGAGAGGGAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAAATA  
 TCTGAAAGTGAAACTCGATCTCTCCGGATATTACCTGTGGAGACCCCTCCTGAGACGTTCTGTGCAATGGGCAATC  
 CCTACATGTGCAATATAGTGTGATGCGAGTACCCCTGAGCTGGCAGACCCCTGAGCTGATGTTTGATTTT  
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT  
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC  
 AAATGATCCTGGAGAACTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA  
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTTGCACAGA  
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTGCGCGCTTTTGG  
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTTT  
 ACAGTCAACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC  
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCCAGGAAGGTGCAAGTGTAATCTCCATGCCACTGTATGTG  
 TGTATGACAACAGCAAAATTTGACATGCGAATGTGAGCACAACACTACAGCTCCAGACTGTGGGAATGCAAGAAG  
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC  
 CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCCTGCCTGCCAGAACGGAGGACGTGCCACA  
 ACAACGTGCGCTGCGCTGTGCCCCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC  
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCGCGACGGCACCCAGCGCTGCTGCTGCTGACCACTGCT  
 GGGAAACCGCCAGCCCCCTGGTGTCTTAGGCTGTCACTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAGCA  
 GACACAACCCAAACATTTGCTACTAACATAGGAACACACACATACAGACACCCCACTCAGACAGTGATACAAA  
 CTAAGAAGGCCTAACTGAACCTAAGCCATATTTATCACCCGTGGACAGCAGATCCGAGTCAAGACTGTTAAATTT  
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCACATTGCCAGCTGCAGAGCATATTGTGGA  
 TTGGAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAACAAATCAACCAGCTAAAAACATTGGC  
 TACTCTAGCGTGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAG  
 GTGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC  
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTTGGTTGAAAGATTTCTTTGCTGATGTTAGTGATGCACA  
 TGTGTAACAGCCCCCTCTAAAGCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA  
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCCTTTGTATTCAAATGAAGTT  
 ATTTTCTTGAACACTGTAATATGTAGATTTTGTATTATTGCCAATTTTGTGTACAGACAATCTGTTAAT  
 GTATCTAATTCGAATCAGCAAGACTGACATTTTATTTGTCTCTTTTGTGCTGTTTGTGTTTCACTGTGCGA  
 GATTTCTGTGAAGGGCAACGAACGCTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGAATAAGA  
 TTCCACCAAGGACATTTCTAAATGTTTTCTGTTGCTTTAAACACTGGAAGATTTAAAGAAATAAAACCTCCTGCA  
 TAAACGATTTTCAAGAAATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTTCACTCACT  
 TTACTGATTTCTGTGTGGACTGAGTACATTGAGTGACGAATTTAGTTCACAGGAAGATGGATTGATGTTCACT  
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAA  
 AAAAAA

**FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCECEHNTTGPDGCKCKKNYQGRPWSFGSYLPIPKGTANTCIPSISSIGTNVCDNELLH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS  
PLVF



**FIGURE 75**

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCGG  
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTT  
 CTCTTGTTGGACCATGTCCTGATCTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC  
 CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGGAATGGAGGAGACGGCTCA  
 AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT  
 AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGCTC  
 AGCAGCCATGGCCTTCTGCTTCTTGAGACCCTGTGGTGGGAATTCACAGCTTCTTATGACA  
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAG  
 AAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGAAAAAAT  
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
 ATGGGGTGATGAATGGTACACACCCGATGCACTGGAGCCTGCTCCTAATTTCCGAATGGAA  
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT  
 CATTCGAGGAGTTCACCTTGCGAAGCATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT  
 TGGACCAAACCTCGTGAAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT  
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGAGCCTGTGGA  
 AAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTTCGGAACATCTGCCCATGTGTATTG  
 ATGGCAGAGCTGTTGCCACAAGCGCCTTTATTTAGGGTAAAATTAACAAATCCATCTAT  
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT  
 GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTGTATCCCCAGGATTCTATTTTGT  
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCAT  
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTACGGTTTTT  
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC  
 TAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATAAATG  
 AGGTGGCTTCAGAAATGGCAGAAATAAATCTAAAGTGTATTATAAAAAAAAAAAAAAAAAA  
 AAAAG

**FIGURE 76**

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF  
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVKW  
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF  
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVKW  
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

**FIGURE 77**

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAGAAAGTGAAGTGGCATT  
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAATAAATTCAGGAGGAGCTCAAG  
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

**FIGURE 78**

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA  
 CCCGACCTTAAAGAGTGGGGAGCAAAGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG  
 CCTGCCCCTTTAAGGGCGGGGCTCCGGACGACTGTATCTGAGCCCGAGACTGCCCGAGTT  
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGCGGCTT  
 CCTCCCCGCTCGTCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGT**A**  
**TG**GGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC  
 GAGTGATTATATCAACACTTCTGTTTGAACACTGTACATCCTCTGCCACATCTTCCTGAC  
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA  
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCC  
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCGTCCGAACTACTACATCCAGTGGCT  
 CAACGGCTCCCCATCCATGGCCTCTGGAACCTTGTTTTTCTCTCTCCCCAACCTGTCCCTCA  
 TCTTCTCATGCCCCTTTCATATTCTTCTACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG  
 GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT  
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT  
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCCTTGGGGTTCTG  
 CTGCTCCTGGTGCTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT  
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCCTTTGAGGAG  
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG  
 CTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC  
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGCTGGTGCTGACGG  
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG  
 CCCCAGGCATGCAAGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG  
 TGCCGTCAATCAGGTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA  
 GCTCTCCACTCTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGAGATAAAT  
 GGAACCTGTGCTGTCTCTCTGGTCCCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG  
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTCTACA  
 TTGTGTTCTCTACAACGAGCCTTTGCAGGCCTCACCACTCTGTCTGGTGAAGACCTTC  
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTGCCGCTGCCGCT  
 CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAG**TGA**CTCCAGCTGGGGGTGGGA  
 AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGCTACTTGG  
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT  
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACCTAACTGTGGCCT  
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCTGATCCCAAATCTGTTTACACATCA  
 ATCTGCCCTCACTGCTGTTCTGGCCATCCCATAGCCATGTTTACATGATTGATGTGCAAT  
 AGGGTGGGGTAGGGGCAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC  
 CTTGCCCTTGCCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG  
 AAAGACCAAGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCAGGGA  
 AAAAA

**FIGURE 79**

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK  
IALELCTFTLAIAGAVLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMF SVTGKLLVKPRLLEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAVIQVVLIFYLMVSSVVGFY  
SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY  
IVFLYNAAFAGLTTLCLVKTF TA AVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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GGCTCGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC  
GCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTCTGTTTGAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTCAACACAGTGGATGATGAAGATGCCACCG



**FIGURE 81**

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC  
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT  
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

**FIGURE 82**

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**CATG**CTGCTGT  
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCATT  
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA  
GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA  
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG  
GCCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC  
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAG**GCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCTGGCATTCCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA  
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**FIGURE 83**

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL  
GKEILRETDPNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

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**FIGURE 84**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT  
 GAGGCGGCTCACAGGGCCGGTGGGCTGGCGAGCCGACGCGGCGGAGGAGGCTGTGAG  
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACC**ATG**GCTCCGAGAACCTGAGCACCTTTT  
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG  
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA  
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG  
 CTGCTTATGAGGTTCTGTGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA  
 GGATTAAGATGGTATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTT  
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA  
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGGAAGTAGTT  
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAACGGAAGTGCAATTGTGCGCAAGAGAT  
 GCGGACCACCCAGCTGGGCGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
 GCCCTAATGTCAAAGTGAATGAAGAACAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT  
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
 CACTTGGATGGTCACAAGGTACATATTTCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT  
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
 CAGCTACTGAAACAAGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGA**GAGTG  
 AATAAAATTGGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
 TTGTGTGTGTTTTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA  
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAATGACC  
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT  
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
 GTTGTGTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGTG  
 TTATTTTTA

**FIGURE 85**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ  
 AQEKFQDLGAAYEVLSDSEKRKQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTFRQQ  
 DRNIPRGSIDIIVDLEVTLEEYVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
 MTQEVVCDCECPNVKLVNEERTLEVEIEPGVRDGMETPFIFEGEGEPHVDGEPGDLRFRIKVVKH  
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLWKKGEGLPNFD  
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

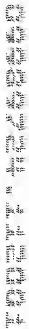
TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNCGCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGGTTTGTAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTTGCTGTGTGNTGNTATACTTCATCGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCTNGAAGTGCTTNTATAAAGGATATTA AAAAGG  
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCTGATGATCCACAAGCCCGAG  
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA  
GTACGATAATTATGGTGAAGAAGGATTA AAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

**FIGURE 87**

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT  
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA  
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**  
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACGC  
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC  
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
 TGGACGATGTCGTTATCACCAACCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
 GAAGATGCCTCGGCTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC  
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
 TACCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAC  
 TCACCTGGTGTGTTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC  
 AGTCTCTGTGCGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG  
 CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTT**TAGT**GCCT  
 ACAGGCCAGCAGCTAGCCATGAAGGCCCCTGCCGCCATCCCCTGGATGGCTCAGCTTAGCCTT  
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG  
 TAAAGCAGGAGATCCCCGTGAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT  
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA  
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT  
 AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG  
 TGTGGCAATTCTGATCTGCATTTTCAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC  
 TTCTTTTGGCAAGACTTGACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT  
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTGCAGGTTTGGGTTTGAAGCTGAGGAACT  
 ACAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG  
 GATAGTAAATTTATACTTATGTTTCCTCAAAAAAAAAAAAAA

**FIGURE 88**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL  
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKSAS  
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI  
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI





**FIGURE 89**

GCTTCATTTCTCCCGACTCAGCTTCCCACCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCC  
CCACCACTGCAGCC**CATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA  
TTTGGAGTGTTTTTCTGTCTTTTGAATGATTCCTTTTTTGGACAAAGCACTACTGGCTAT  
TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATTGGTTTAGAAAGAACATTCAGAT  
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTC  
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG  
GGGCTTCTTCTGTCTGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT  
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTA**TAA**CAACA  
AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA  
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTCTTTACAGGAGTTTAAACGTATAG  
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAAAGGCTTCTACTCAAGTGA  
ACTAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
CTGTGGTGCCTGTTTCTTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT  
TTTTAGAAGTGCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA  
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAAACCCCAATTTTG  
ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

## **FIGURE 90**

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI  
RSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

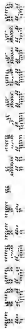
amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites.**

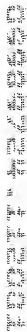
amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59



GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTCTCCCGACTCAGCTTCCC  
ACCNTGGGCTTTCGAGGTGCTTTCGCCGTGTCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTCCTGTCTTTGGA  
ATGATTCTCTTTTGTACAAAGCACTACTGGCTATTGGAAATGTTTATTGTAGCCGGCTT  
GGCTTTTGTAATTGGTTTAGAAAGAACATTAGATTCTTCTTCCAAAACATAAAATGAAAG  
CTACAGGTTTTTTCTGGGTGGTGTATTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG  
ATCTTCGAAATTTATGGATTTTTCTCTGTTC



**FIGURE 92**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA  
 GGCTGCCAGGAAGGAGACGCCCTTCTGAGTCTTGGATCTTTCTTCCTTCTGGAAATCTTTGA  
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATGG**ACCTCGCGGGACTGC  
 TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGTACGCTCTTTATGCTCAGGGCTAATC  
 ATCAACACCATTACGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT  
 CGGGCACGGAATGCACCATCTTACGACCCGCGCGCTACCTCAAGTATGGAAGGAAAAT  
 GCCATCGTGGTTCTCAACCACAAGTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA  
 TTATCGGCTGGATGTGGTACTTACCCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT  
 CGCAAGACGGTGGCCACAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT  
 GATTCACGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC  
 GGGCCAAGGGGCTGCCTCGCTCAAGCATCACCTGTTGCCACGAACCAAGGCTTCGCCATC  
 ACCGTGAGGAGCTTGAGAAATGTAGTTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA  
 TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGAAAGAAAATACCATGCAGATTTGTATG  
 TTAGGAGGATCCCCTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC  
 AAGCTCTACCAGGAGAAGGATGCCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCGA  
 GACGCCCATGGTGGCCCCCGGGCGCCCTGGACCTCGTGAAGTGGCTGTTTTGGGCCTCGC  
 TGGTGCTCTACCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGTCTTCCCTGACG  
 CTGGCCAGCTTCATCCTCGCTTCTTTGTGGCTCCGTGGGAGTTCGATGGATGATTGGTGT  
 GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGAC**T**  
**G**ACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCTCTGCATATCCT  
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA  
 CCTCTCCAGCCAGGAGTCTGGTCTCAAGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT  
 TTTTCCCATGTGCTTTAGTGGGCTTTGGTCTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC  
 TGTGTGGTGAAGTGTGAACCTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGAG  
 GGCAGGGCTGGGGACCAAGGGGACAAGTCCCCCTTATCCTTTGGTGCTGAGTTTTCTGT  
 AACCTTGGTGTGCCAGAGATAAAGTGAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC  
 CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

MDLAGLLKSQFLCHLVFCYVFIAASGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV  
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLGGSKVLAKK  
ELAYVPIIGWMWYFTEMVFCSRKEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHLLPRTKGFAITVRSRLNVVSAYVDCTLNFRNNENPTLLGVLNGKK  
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS  
KQKLN

**FIGURE 94**

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG  
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA  
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCTCAAAATGGATGATGTTGAAGTTGTTTA  
 TACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG  
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAAATGTCAAAAAGAATGTGGTAGGT  
 TGGTACAAATTCGGTCGTATTGATCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA  
 AAACCTTGAGGAGCATTTTTCAAACCAAGACCTGTTTTTCTGCTATTAAACACCAAGTATAA  
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT  
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTGAACAACTGGGTATATAAAC  
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT  
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA  
 CAAGAGGAATTAAGAGATATATGCAAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAAT  
 AGTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG  
 CAGCAAGAGAGAAGAACATCCAAAAAGACCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA  
 CGGACCTTTTTTCCAAATCTGAATTTCTTCATTGATGTGTTATGTCTTTAAAAATAGACA  
 TGTTTCTAAAAGTAGCTGTAACACTACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA  
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT  
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA  
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC  
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA  
 TTT**TGA**TCTCTTTTAAACCTTACAAGGAGATTTTTTTATTGGCTGATGGGTAAAGCCAAACAT  
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTTCATTTGTTTTTACTATGTTTAC  
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC  
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTCTACTAAGTTGTTGAGGGGAAGGCT  
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA  
 TCCCAGCACTTAGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC  
 TGGGCAACGTATTGAGACCATGTCTATTAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT  
 TTTCAAAATATGGAAGAAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAG  
 TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA  
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHNLNTSDTEGFLLEGVKGEAKNSITDSQMDDDEVVYITIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKILSNVKNVVGWYKFRRHSDDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTRLEHSLYKPQKGLFHRVPLVLANLGMSEQLGYKTVSGSC  
MSTGFSRAVQTHSSKFFEEGDGLKEVHKINEMYASLQEELEKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS  
CNYNHHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLLDTDQDKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

**FIGURE 96**

GGCACAGCCGCGCGCGGAGGCGAGAGTCAGCCGAGCCGAGTCAGCCGGACGAGCGGACGAGCGCAGGGCAGC  
 CCAAGCAGCGCGCAGCGAAGCCCGCGCGCCACACCTCTGGGGTCCCCGCGGGCGCTGCCACCCCTCCCT  
 CCTTCCCCGCGTCCCCGCTCGCCGGCCAGTCAGCTTGGCGGGTTCGCTGCCCGCGGAAACCCCGAGGTCACCA  
 GCCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCGCTCCACGCGCTCCTTCTCCCTGGCCCGCGCGCTGGCACC  
 GGGGACCGTTCGCTGACGCGAGGCGCCAGCTCTACTTTTCGCCCGCGCTCTCCCTCCGCTGCTCGCTCTTCCAC  
 CAATCCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAG  
 CGCCGCTTCCCGTCCCGTCCCAAAGGTGGGAACGCGTCCGCCCGCGCGCCGACCATGGCAGCAGGTTTCGGCTTGC  
 CGCGCTTCTCTGCACCCCTGGCAGTGCTCAGCGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG  
 AAGTGCAGCGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT  
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA  
 TGATTTCAAAGTGTGTGTCAGCGAACAGTGCAATCATTGGCAAGCTGTCTTTGCTTACAGTTACAAAGAGTTTG  
 ATGAATTTCTCAAAGAATACTTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT  
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTTGGTGGAAATGT  
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTTGGTGAACCTCCAGT  
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT  
 CGCAAATGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTTCTCAAGGCTTAGCGGTTGCGGG  
 AGATGTGTCGAGCAAGGTCCTGGTGAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT  
 GCTCCCACTGCCGGGGTCTCGTGACTGTGAAGCCATGTTACAATACTGCTCAACATCATGAGAGGCTGTTTG  
 GCCAACCAAGGGGATCTCAATTTGAATGGAACAATTTTCATAGATGCTATGCTGATGGTGAGAGAGGCTAGA  
 GGGTCTCTTCAACATTTGAATCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG  
 ATAAATAGTGTTCAGTGTCTCAGAAGGTTTTCAGGAGTGTGGACCCCCAAGGCCCTCCAGCTGGACGAAT  
 TCTCGTTCCATCTCTGAAAGTGCTTCACTGCTCGCTTCAGACCACATACCCCGAGGAACGCCAACACAGC  
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATTTCTGGTCTT  
 CCCTTCGAGCAACGTTTGAACGATGAGAGGATGGCTGCAGGAACCGCAATGAGGATGACTGTTGGAATGGG  
 AAAGGCAAAAGCAGGTACCTGTTTTCAGTGACAGGAAATGGATTAGCCAACCAAGGCCAACCAACCAGAGGTCCA  
 GGTTGACACCGACAAACAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA  
 AGAATGCATACAAATGGGAACGACGTGGACTTCTTTGATATCAGTGATGAAAGTAGTGAGAAGGAAGTGGAAGT  
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTGACTACAAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGA  
 GAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCACAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGG  
 TTATCGCAGAGAGTGGAGATTAATTTCTCAAACCTCTGAGAAAAGTGTTTCATCAAAAAGTTAAAGGCACCAAGT  
 ATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTTCTATGTGGC  
 CACTGGTTTAAAGAGTGCTGACTTTGTTTTCTCATTCACTTTTGGGAGGAAAAGGCACGTGTCATTGAGTTGGT  
 TCCTGCTCCCCCAAACCATGTTAAACGTGGCTAACAGTGATGTTACAGAACTATAGTTAGTTGTGCATTTGTGA  
 TTTTATCACTCTATTATTGTTTGTATGTTTCTCATTTCGTTTGTGGGTTTTTTTTTCCAACTGTGATCT  
 CGCCTTGTCTTCTACAAGCAAACAGGGTCCCTTCTTGGCAGTACATGTACGATTTCTGAAATATTAAATA  
 GCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAAGAAAAGCCCCAAAAGC

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**FIGURE 97**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ  
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF  
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEMLNDFWARLLERMFRVLVNSQYHFTDEY  
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSNNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES  
VMDPIDVKISDAIMNQDNSVQVSQKVFQGC GPPKPLPAGRISRSISESAFSARFRPHHPEE  
RPTTAAGTSLDRLVTDVKEKLQAKKFWSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYL F  
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE  
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**FIGURE 98**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT  
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA  
GCAACTTACAGCTGCACCGACAGTTGCCATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC  
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC  
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA  
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC  
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA  
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTGAGCTAAGAAGCTT  
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTCCAATTAAACATTCTCAGCCAAGAA  
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC  
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTTGCTCTC  
TCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT  
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCTTAGCTAGTGTCAATTAACCTTAAATGC  
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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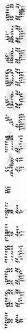
**FIGURE 99**

MKVLISSLLLLPLMLMSMVSSSINPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR  
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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**FIGURE 100**

AATGGCTGCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT  
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA  
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA  
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACAAACAGAACTCATTTTGAACACC  
CTGACTGCATTTTTGCTTTTAGAAAGTTAGAATAAAATATGGCGCTTTGGGATCACATAGTTG  
ATGGAGAGGAAA



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**FIGURE 101**

MAVLVLRRLTVVLGLLVFLTCYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIIENAVE  
FILRSMRSRSTGFMEFDDNEGKHSSK

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**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAGGCCAGTGCCCCAGCGGAAGCACAGCT  
CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCACTCCTGCAGCTGCTGGTCTGCTTCTTAC  
CTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC  
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG  
CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC  
CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
GGTGGTCTGCACCTCTGGTCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC  
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
AGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCACCTGGAAACACATTGGGGATGGCTG  
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAAGTTCTCCGAAATCCAAATGG  
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA  
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT  
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC  
CCGCCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC  
TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC  
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT  
CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT  
CTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT  
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTTTAATAAATAGACGA  
AACCACG

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**FIGURE 103**

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELF SQI  
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV  
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGVLF FWEHV AEPYGSWAFM  
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP  
SSKALICSFPSLQLEQATHQPIY LPLRGT

**FIGURE 104**

GTGGGATTATTTGAGTGAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG  
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA  
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG  
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTTG  
 TTAAGGAATGAGGTTACAGATTACAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA  
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG  
 AAGACAGGCTTGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT  
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG  
 TGATTCCCTGAAAGCATCAGATACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAA  
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC  
 TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA  
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG  
 AAGATTGTGATTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC  
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCTGAAGCTTTCCATGAAAGCCAGCACTTG  
 CTCATTTAATCCTGGAGTTTTTGTGTGCAAACCTGACGGAATGGAACGACAGAATATAACTA  
 ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT  
 GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC  
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAACGATATTACCTCAGTTTGTA  
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGAAGGACTGCTTCATAT  
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAG  
 ATATACCGAGATCTCAAACATAAAGTGAACAGAATTTGAACTGTAAGCAAGCATTCTCAG  
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
 GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGTC  
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTCCTT  
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA  
 TAATTCAAAACCTGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAATAAACTT  
 ACATTTTTTC



**FIGURE 105**

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR  
QEEIPVVIAASEDRLGGAIAAINSIOHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK  
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT  
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA  
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRHLGS  
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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TGGTTTTTGGCCCATAAATTCCCTCAGCTTGAGCAGTTTGTGAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAATGTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT  
TGCAGCTATAAACAGCATTGAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACTTTGCAAGGTTCTACTTGCCAATCTGGTTCCAGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

**FIGURE 107**

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGCTGCGCGGCTGCCACG  
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC  
TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGGGGCTGCA  
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGCGAGCCTTTGAGGGGAACGACT  
TGTCGGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT  
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT  
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTAGGAATTGTAG  
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA  
ACAGCATTCAAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA  
GCAGACCATCTCCGGTCTCGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG  
TCAATTTTGACCCATAACTTTTGGAAGGAAAAGTAAAGGAGGATCTGACCAGGGGGAATCC  
ATGAAACCTTTAACTTTTGCAAGGTTCTACTTGCCAATTTCTGGGTTCCAGCGCAAGAAGG  
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA  
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT  
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA  
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTGTGTTGCAAAC  
CTGACGGAATGGAACGACAGAATATACTAACCACCTGGA AAAATGGATGAACTCAATGT  
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG  
TATTTTATCAACAGCACTTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTCCAGT  
GCTGGAAAACGATATTCACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGA AAAATGGTATATTCCA  
GACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA  
CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG  
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGA AAAAGATGTGTCAGCTAG  
GTAAAGATGACAACTGCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT  
ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA  
CTGATATGGCTAGTTCACTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT  
GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTTCAATAGGTAAAAA AAAAAA  
AAAAAA

**FIGURE 108**

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT  
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG  
TCTGTGCTGGTCTGAGGGTGCTGCCTGT**CATG**GGGGCAGCCATCTCCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG  
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC  
TGGCCCCTGTCCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC  
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACC**TAA**GTCCACCTCACCTAGAG  
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC  
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCAG  
GCTGGGGCCCTCCCCTGGTCCTCCAGTGTTTGCTGGATAATAAATGGAACATATGGCTCTAA  
AAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLLWVILCWACHSRLPTLTLNLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGWPSPLEPRT

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

**FIGURE 110**

GTTGAATTCCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA  
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATTCAGTGGA  
 TC**CATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC  
 ATGATGTTTACCTTCAGATTTCATCACCACCTTCTGGTTCACATTTTCATTTTCATTGGTTAT  
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
 TCAGCATAGAATTGGACACAGAAAGGGAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA  
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT  
 GACAGTTGAGCTTTTCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCC  
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCCTCTGGGTGGCTGTGCTGCTG  
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCCT  
 TTCGGGCATTCCGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTC  
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGTTACTTGTTATTTCAACAGAAGT  
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA  
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTTGTCA  
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA  
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT  
 TGTCGAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTCTA  
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG  
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC  
 ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT  
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGCACAGCAGGACAAGCACTCATTAAGGA  
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGAT**TAG**ATACCCATTTAGGTATCTGTACCT  
 GGAAACATTTCTTCTAAGACCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT  
 AGTGAATTTTTTTTTAAAGACCTAATAAACCTATTCTTCTCCTCAAAA

**FIGURE 111**

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDL  
SIELDTERENMKCVLGFIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLN NARAQQDKHSLRN  
EEGTELQAIVR





**FIGURE 113**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC  
PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL  
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ  
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ  
RQDPSGAAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSTRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVCDTDRLACSKTCLNSADI  
GFVIDGSSSVGTGNFRTLQFVTNLTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPDIL  
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG  
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

**FIGURE 114**

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCT**A**  
**TG**CTTTTCCGGTGCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATTGGT  
 GCGCCAGGTCCCAGCGGTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT  
 TGATGCACTGGACACCTTGCTGATTTTGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG  
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCTCTGTGTTTGAAACAAACATT  
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA  
 GGCTGGATGGCCCTGTTCCGGGCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACTCC  
 TCCAGCCTTTAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG  
 AACCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
 CACCCTGAGCAGCTCACTGGTGACCCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC  
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC  
 AAGTGGGTGGCCAGGACGCGAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT  
 GAAAGGAGCCATCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG  
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTGAGATGTACAAGGGGACT  
 GTGTCCATGCCAGTCTTCCAGTCCTTGAGGCCTACTGGCTGGTCTTCAGAGCCTCATTTGG  
 AGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGTATGGAAGCAGTTTGGGG  
 GGCTCCCGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA  
 CTTCCGCCAGAATTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGATCCCACCCT  
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT  
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG  
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG  
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGATCCTGGGGGCTGGGGGGTACA  
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG  
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC  
 GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC  
 TCTTCTCACCAGAAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA  
 CTTCTCAGTGTCCCGAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT  
 AGACTCCTC**TAA**CCACTGGATAATTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA  
 AATTGCTTTTGGCTATCATAAAA

**FIGURE 115**

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPILLMAEEAARKL  
LPAFQTPGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSL EAYWPGLSLIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG  
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY  
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRKFQKNTVSSGPWEPPARPGT  
LFSPENHDQARERKPAKQKVLLSCPSQPFTSKLALLGQVFLDSS

AAGGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTCTGGGCCGGCTCTAGAACA  
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGCCATTCTGCCTGCCCTCAGAACCTC  
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA  
 AACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC  
 ACGGCCACTGTGCCATACAACCTTCGTGTCAAGGCCACATTGGGCTCACAGACCTCAGCCTG  
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTT  
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
 GGGTATTCCAGTGCACTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA  
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCTTTGTTGGCTTCATGCTGATCCTTGT  
 GGTCTGTGCCACTGTTCTGTGGAATAATGGGCCGGCTGCTCCAGTACTCTGTTGCCCCGTGG  
 TGGTCTCCAGACACCTTGAAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG  
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
 CTCATTAGGTTTGCGGAAGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC  
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA  
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG  
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
 GGCTTGAGAGAGCCACTTCCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
 TGTTGAGTTCACCTTCAAGCCCAATGCCGGTGACAGGGGAATGGCTTAGCGAGCTCTACAGT  
 AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
 CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
 GTGCAATGCCAGCAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTTC  
 TGTTGGTAAAGTACAGAATTACGCAATAAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA  
 AAAAAAAAAA

**FIGURE 117**

MQTFTMVLEEIWTSLFMWWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILILV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-43 and 134-137

**Tissue factor proteins homology.**

amino acids 92-119

**Integrins alpha chain protein homology.**

amino acids 232-262

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTAATCTGTGCGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCTTGCGGCGCAAGGG  
GTTCGCGAACCCTTGCGGCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

**FIGURE 119**

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCCATGGTGGCGGCGACGGTGGCAGCGGCGTG  
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG  
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGGGATCGGTGTCCCTGGTGGTG  
AATGTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG  
AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCTGCAACCAGTTTGGCCAACAGG  
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCGCACCTACAGTGTCTCATTCCCC  
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA  
GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG  
TGGTAGGGGCTTGGGACCCAACCTGTGTGTCAGTGGAGGAGGTGAGACCCAGATCACAGCGCTC  
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAACACCGCGTCTCCTCCTCCACCA  
CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG  
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA  
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG  
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAA  
TAGAAGTATATCAAGCAATAATCTCCCACCAAGGCTTCTGTAAACTGGGACCAATGATTAC  
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC  
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAAT  
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT  
GTTATTTCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA  
AACAAATACCTCACGATATAAAATAAAAATGAAAGTATCCTCCTCAAAAA

**FIGURE 120**

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLSEKYRGSVSLVNVVASECGFTDQ  
HYRALQQQLQRDLGPHHFNVLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG  
AHPAFKYLAQTSGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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**FIGURE 121**

CGGACGCGTGGGCGGGCCGGGACGCAAGGAGCG**CATG**GCCTGTCTACGTCCGGGATGC  
 TGGCGCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCCCGGGCCGCCCTCTCT  
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATCG  
 CATGGTCTCCACGCCCATCGGAGGCTCAGCTACGTTCAAGGGTGCACCAAAAGCATCTTA  
 ACAGCAAGACTGTGGGCCAGTGCCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC  
 TTGGTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCAACTCAAGGAGGAGGTGGACAA  
 AGCTGCTTCTGGCCCTCCTGAGCATTTGGCCCTGTGCAAAGGTGACCGCTGGGCATGTGGGGAC  
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCAGGCATCATTCTGGTG  
 TCTGTGAACCCAGCTACCAAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA  
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT  
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCCAGATCTGACC  
 ACAGTCATCTCGGTGGATGCCCTTTGCGGGGACCTGCTCCTGGATGAAGTGGTGGCGGC  
 TGGCAGCACACGGCAGCATCTGGACGCTCCAATACAACCAAGTTCCTGTCTGCCATG  
 ACCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCTCTCC  
 CACTACAACATTGTCAACAACCTCCAACATTTTAGGAGAGCGCTGAAACTGCATGAGAAGAC  
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTTGCCTGGGTCCGTGGCAG  
 GCACAATGATGTGTCTGATGTACGGTGGCCACCTCATCCTGGCCTCTCCATCTTCAATGGC  
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCAACGAT  
 GTTCGTGGACATTTGAACACGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG  
 GTGTCAATTGCTGGGTCCCTGCACTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT  
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCGTGACATTCGCGCACTT  
 CCTTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGG  
 CCCGGATCATGAACATGGAGGCAGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC  
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT  
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA  
 AGATCGTGGGCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG  
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA  
 CGATCGGATGGGGGAAGAGATTTGTGCTGCAATTCGGCTGAAGGACGGGGAGGAGACCACGG  
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCGAAGTACATC  
 GTGTTTGTCAAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA  
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCTGTCTGGCCGTTGGCTT  
 GACTCTCTCCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTC  
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAATAAGAGCTCCTGGATGGGTC  
 CGGGAATCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG  
 TCCATCCCCACATCCCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT  
 GAAAAAAAAAAAAAAAAA

**FIGURE 122**

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFSSREVD RMVSTPIGGLSYVQ  
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY  
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTILLDEVVAAGSTRQHLDQLQYN  
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY  
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG  
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGADVAT  
MNEQGFCIKIVGRSKDMIIRGENIYPAELEDFHHTHPKVQEVQVVGKDDRMGEEICACIRL  
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCTGGCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC  
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCCTCACACGGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

**FIGURE 124**

GAGCAGGACGGAGCC**ATG**GACCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC  
 AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGC  
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGTGCGC  
 AGTGCGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC  
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC  
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCGTGGAGTG  
 CTACAGCTGTGTGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGTAGCT  
 GCTACAACGCCACGGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA  
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGACTCGGGA  
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT  
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCCGGCTGCCCCCT  
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACCTTCTACCTCGGCCCCAGTGAG  
 ACCCACATCCACCACCAAAACCCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG  
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC  
 CGCAGCAATTTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG  
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGTTGCTCCTACTG**T**  
**GA**GCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
 CATCACTTCTGTTCCCACTGGACTGGGCTGGCCAGCCCCTGTTTTTCAACATTCCC  
 CAGTATCCCACTTCTGCTGCGCTGGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT  
 ATTCTGCCAGGGGTGTTCTAGCTTTTGGAGACAGCTCCTGTATCCTTCTCATCCTTGTCTC  
 TCCGCTTGTCTTCTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG  
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG  
 GGTGGGTGGGACAATGGCTCCCACTCTAAGCACTGCCTCCCTACTCCCCGATCTTTGGG  
 GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCGGTAC  
 CCAATTCGCCCTATAGTGAGTCGTA

MDPARKAGAQMIIWTAGWLLLLLLRGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT  
EAVGAVETIHGFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQCAQDRCAKLNLTSLRAL  
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSVCYNASDHVYKGCDFGNVTLTAAVNTV  
SLPVRGCVQDEFCTRDGVTGPGFTLSGCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT  
VASTTSVTTSTSAVPRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRNSNG  
QYPAKGGPQQPHNKGCVAPTAGLAALLAVAAGVLL

[illegible]

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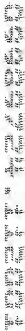
**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK  
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTQVQPSGGSLWNLRRLLEPLDANVDA

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**FIGURE 128**

AAACTTGACGCC**CATGA**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCTACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT**G**  
**GACC**ATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACCTCAATAAAACATTTTCCATCCAAA





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**FIGURE 129**

MKIPVLPVVLLSLLVLHSAQGATLGGPEESTIENYASRPEAFNTPFLNIDKLRSFAKDE  
FLNWHALFESIKRKLPFLNWDAFFPKLKGLRSATPDAQ

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**FIGURE 130**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCCATGGGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT  
TTCTCCAGCCAGTTCCTCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGCCACTCCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT  
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA  
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCTTTATTTTT  
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC  
TTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA  
TGTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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**FIGURE 131**

MGVEIAFASVILTCLSLAAGVSQVLLQPVPPTQETGPKAMGDLSCGFAGHS

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MGVEIAFASVILTCLSLAAGVSQVLLQPVPPTQETGPKAMGDLSCGFAGHS

**FIGURE 132**

GGGGAATCTGCAGTAGGTCTGCCGCG**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG  
 GCTGCTGTTGTTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA  
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAC  
 TGCAGCTGCTACCATGGTGTACATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
 GACTGTACCGGGAATAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT  
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT  
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGACGAGCACAGTG  
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
 ATCCTCTCATTTCTGTCTCGGAAAAACCCAAACTTGTGTATGCAGAATACACCAAAAC  
 CAGGCCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
 GGATCACTGCAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
 AACACCTCTTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTTTC  
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA  
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA  
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTTTG  
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT  
 TCCCAAAATGTTGAAAAGTGAAGT**ATAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA  
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA  
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA  
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCAATTTCTTAAGACCAATC  
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA  
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA  
 CTCATTGCTGGAATTGTGAAATTATTCAGGCGTGATCTCTGTCACTTTATTTAATGTAGG  
 AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG  
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCATAAACTCTGTTACTCAG  
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
 TCAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAA

**FIGURE 133**

MEWWASSPLRLWLLLFLLP  
SAQGRQKESGSKWKVFIDQ  
INRSLENYEPCCSQNCSCYH  
GVIE  
EDLTPFRGGISRKMAEVVR  
RKLGTHYQITKNRLYREND  
CMFPSRCSGVEHFILEVIG  
RLPD  
MEMVINVRDYPQVPKWME  
PAIPVFSFSKTSEYHDIMY  
PAWTFWEGGPAVWPIYPTG  
LGRWDL  
FREDLVRSAAQWPWKKNST  
AYFRGSRTSPERDPLILLS  
SRKNPKLVDAEYTKNQAWK  
SMKDT  
LGKPAAKDVHLVDHCKYK  
YLFNFRGVAASFRFKHLF  
LCGSLVFHVGDWLEFFYP  
QLKPWVH  
YIPVKTDLSNVQELLQFV  
KANDDVAQEIAERGSQFI  
RNHLQMDDITCYWENLLS  
EYSKFLSY  
NVTRRKGYDQIIPKMLK  
TEL

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**FIGURE 134**

CACCCCTCCATTTCTCGCC**ATG**GCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT  
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT  
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA  
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC  
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG  
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTGCAGCTGGTGATGCGGTACTGGGAGCC  
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC  
 TCCTCTGCTTTGTGCTCCATGTCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT  
 GACTATGCTGAGCTCATGGGCCCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC  
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG  
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT  
 TTCCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT  
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGCCCCAGGATGGGGAGGCAGAG**T**  
**G**AGGAGCTCACTCTGGTTACAAGCCCTGTCTTCTCTCTCCCACTGAATTCTAAATCCTTAAC  
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCAAATCCATGGACTGAAGGAGATGCCCCTT  
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA  
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC  
 CTGACCACTCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCTTCTGCACCGCT  
 GGCTTCCACTCCAAGAAGGTGGACCAGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA  
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT  
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAAGTTCGATGACTTGGGGCTC  
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTCTAAAAAAA

**FIGURE 135**

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP  
LAWDLGLLLLFVGQHSILMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV  
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP  
RALRLEFSLRHFPVCVELLTVLWVVP TLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR  
KLHLLSRPQDGEAE

**Signal sequence:**

amino acids 1-13

**Transmembrane domains:**

amino acids 58-76, 99-113, 141-159, 203-222

**N-myristoylation sites:**

amino acids 37-43, 42-48, 229-235

**FIGURE 136**

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTCTAGAGTAGTTCACAACAGATCTGAGTGT  
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAAGCTTAAATTCATCTGGAATT  
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCCTCGGCTCGCGTGCTTCTG  
 AGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACCTGAGATCC  
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT  
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT  
 ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT  
 CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG  
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT  
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC  
 ATTACAGTGGGTAAGTACTGAGTTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT  
 TTCACAGGTTATCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT  
 TTCTTACCAGGAGTATCCTTTCAAGGTGTCCCTCCATACTGCAGTGGGTTGGGTTATATAA  
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCCATCAAGTTT  
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTATATCCAGAAGA  
 CACAAATCTTTTCTTTCTATATAGAATCCATTGGATGTCTGTCAACTGAGACGTGTGATTG  
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTCATGCTAAGGAACACC  
 ACATGCCATTATTAAGCTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGAAA  
 GTGTTAAATAAAGTAGGTACTGTGGAATAATCATGGGGAGGTGAGTGTGCTGGCTTACACTG  
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTACACTTGTGATTTATTAGTC  
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTCTAAA  
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG  
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAACAATGTAGAGTTTATTATTATG  
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA  
 TGTAGTTCTGTGTCAAAAACCTTCTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT  
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA  
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCATACAAGATAAAAAGGATAGTGAAT  
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTAAAT  
 ATTTTACTGTGGTAATATAGAGAAGAAATTAAAGCAAGAAAATCTGAAA



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**FIGURE 137**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQD  
FHFTTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLGQEA EK  
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTlKTIMAFRWVTEFCPNAKYVMKTDTDVFIN  
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQ EYPFKVFPYCSGLGYIMSRD  
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNlHIPEDTNLFFLYRIHL DVCQLRRVIAAHG  
FSSKEIITFWQVMLRNTTCHY

**FIGURE 138**

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT  
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

## **FIGURE 139**

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS  
IWDYGNNGFAATRLFKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN  
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

### **Signal Peptide:**

amino acids 1-20

### **N-myristoylation Sites:**

amino acids 67-72, 118-123, 163-168

### **Flavodoxin protein homology:**

amino acids 156-174

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**FIGURE 140**

CATTTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA  
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG  
 CTCATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT  
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA  
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTGTTTACATG  
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTAC**ATGA**AATGACAGTCTTCGAACCAATGTGT  
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT  
 CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT  
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC  
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCCTTACAAGAAGCCAAATTAAAGCAAGGGGA  
 TTGAATCCGGATGGAAGCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC  
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG  
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAGAAAA  
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG  
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA  
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT  
 GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAACAGACATGG  
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG  
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
 GAGAGGTCCCATAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG  
**CTGA**CTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGTTTTGCCTATCTACAGTGTGATGT  
 ATGGACTCAATCAAAAACATTAAACGCAAAGTATTAGGATTTGATTTCTTGAAACCCCTCTA  
 GGTCTCTAGAACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT  
 AAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTCAATTTGACTTTATTATAGT  
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT  
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT  
 ACTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTTTACAAGGAAATAAAATACAAAT  
 CTTGTTTTTCTAAAAAAGT

**FIGURE 141**

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY  
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK  
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN  
NRRSRSGTYSSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ  
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNATATTCGGGTCAANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT  
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGC  
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATNTTATTGCTTACTGATTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAAGAAAAAGCCAACTATGAATTACTG  
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT  
GAATCCGGATGGAACCTCAGCCCTTTCAACCTGGGTGGATTTTCTCC

GGACACGAGGCGCTCGTGCCAAGCTTGGACACGAGGCTGCACCGCTTCTCGCACGCGCTC**ATGGC**  
GGTCTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC  
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGACCCG  
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG  
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG  
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG  
TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTACAGAGGCCTACTACTACAT  
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTCTGCTGCTGCTCACGGTGACCTTCT  
CCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC  
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG  
GGAGGAGACCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCAGAAGTATAGAGC  
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG  
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCCAGGCCTGCGGCTGGC  
CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC  
ACACCAGCTTCTGTCTCCCTGTTCATCTGTGGCTCTGGACAAAGCCCATTCACGGGAC  
TTCTTGCAACAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA  
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGCTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC  
ACCTGCAAGCCTACCTGTGCTTGGCCAAGGCCCGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
GAGCTTGCAGTACCTGACGCGCTCATCTTCAACCTCAACTGCACACTTCTGTCTAAGACGC  
TGGGAGGCTATTCTGGGGCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCTCTAGCC  
AGCGTGTCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG  
GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT  
GGACGGCTGCCTGCCAGTGCTCGCCAGCCTTTTCGGCCTCTACTTCACCAGCACTTGCA  
GGCTCCT**TAGC**TGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTCTCTGGGGCAGCGGACA  
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCAGCTGCAAGGTGGGGCCGAGTCTCCC  
GGCGTTCCTTACCACAGTGCCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA  
GAAGTGTCTCTCTGGGCCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG  
TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTTCTGAACAAATAAAGGAGCATGCC  
GATTTTAA

**FIGURE 144**

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE  
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY  
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGGERSVCLTFAFLFLLAMLVQV  
VREETLELGLPEGLASMTQNLEPLLKKQGDWALPVAKLAI R VGLAVVGSVLGAFLTFFPGLR  
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA  
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT  
VVS LQYLTP L I L T L N C T L L L K T L G G Y S W G L G P A P L L S P D P S S A S A A P I G S G E D E V Q Q T A A R I  
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLA GS

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**FIGURE 145**

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT  
TGTTCGATAACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC  
TTCTTCCTGGAGTACCACTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCCTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCTGCTGCTGGC  
CATGCTGGTGCAAGCG

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GTTCTCCATACCTCTCTCATCTGAGAAATCAGAGAGACATATCTTCTACGGCCGCGTGATTTAATACGTGGCT  
 AATTCAGAAGGTTCTGACATCAAAATCTTTTGATCTATGATTGTGGGGGACATGCGAAGATTTGCTTAAGAGGAC  
 TTGGCTTGGTTTGGCGGCTTTGTAGCTTGACAGAAGGTGGCCAGGAGAAATCAGCACACATGCTCGGAGAATGAAGAAG  
 CGCTTTCTTTGCTGTGCTTTGCTGCTTGGCTCAGTCTGCTGATACATACATGCAATGTGGGCAACCTGCATCTCTCTG  
 TATTCAAGAATCTGTAAAGGTGCTCCCATACGGCTGACCAAGAGTAGGAAGAGGCGCTCACAGATGGCTG  
 TCAGACAGCGCTGTGGCAGCTCTCAGACGACCGGCTCCTCCCGCAGAGTTTTCGAGCTGCCAACCTCTCCTTAA  
 TCAGACAGAGCGCTGGCTTCAGACAACTCGCTACGTGTCTTCGCGAGAGCAGGGCAGCGACGAATCAGCCG  
 GTGGACTCTGGCCGAGACCAAGCAATAGGCGACGGCCCTTGAGAGATGTCACATTATTAAGCAGCATATTTA  
 AAAAAATAATCAGCTTTTGATGTTCTTTCCAGGAACCAAGCCAGGCGGAGTGCATTTGCCAACTGCCGACGG  
 GCAGGGAAAAATCTGAAAACACCCTGCCCTGAAGTCTTTCCAAGTTGTACCACCTGATTCCAGATGGTGAA  
 ATTACAGCATCAAGATCAATCGAGTAGATCCAGTGAAGCGCTTATTATAGGCTGGTGGGAGGTAGCGAAGC  
 CCACTGGTCCATATCATTTACCAACATATTTCTGATGTGGGTGATCGCGAGAGACGGCGGTATCTGCCAG  
 GAGACATCATTTCAAAAGTCAACGGGATGGACATCAGCAATTCCTCCACAGTACGCTGTGCTGCTCTCTCGGG  
 CAGCCCTGCCAGGTGCTGTGCTGATCTGATGCTGCACAGAAGTTCCGCAAGAGAAACATGGACAGGCCG  
 GAATCTGCTACAGACCCGAGATGACAGCTTTCTGTGATTCTCAACAAAGTGTGCCCGGAGGACGCTTGGAA  
 TTAACCTGGTCGCGACCGATGAGCTGAGCTGGGCTTATCATCTTCAATGCTGGATGGCGCTGTGCACTTCGA  
 CATGGTCAGCTTGAGGAGAAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCGAGAAAG  
 TGGCGGCTCATCTGATTGACGGCCAGTGAAGAGCGTGTTCACCTCGTGTGCTCGCCGAGGTTCCGCGAGGCGG  
 CTCGACATCTTTCAAGAACCGCGTGGAAACGCAATGGACGCTGTCCCGAGCGCCAGGGAGAGGAGCAACT  
 CCGAAGCGCCCTCGCATCTCAACATTACTTTGTCTGATGAGAAAGTGGTAAATATCCAAAGAGCCCGGTGAATCTC  
 CCGATGACCGCTCCGAGTGGGAGCATCATATGAGAAATGGATTTGGCTATCTATGTCATGATCTTATGCGCG  
 GAGGATGATAAGCAGATATGAAGAAATAAAACAGGTGACATTTGTTGATATGTGATGGGTGGCACTGACA  
 GAGTCAGCCGGAGTGAGGCATGGCATTTATGAAAGAACTATCATCTCTGATGACTCAAGCTTTGGAAGT  
 CAAAGAGTATGAGCCCCAGGAAGACTCGACGACGCCGACCGCTGGACTCCAAACCAACATGGCCCCACCA  
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACACGGTGTCTGTATACCTTGAAGATATTTGATTA  
 CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCAATTAGGAGGTTATGAAGATACAATGAAAGCAAACTTT  
 TTTCTCATCAATCTGATTTGAGGAACAACAGCATCAATGATGGAAGAAATAGATGTGGTGATATTTCTTTG  
 CTGTCAAGTGTAGAGTACATCAGGAATGATACATGCTGCTGTGCGAAGCTGCTGAAAGCAATCAAGGA  
 ATTACTCTAATCTATTGTTCTTGGCCTGGACATTTTATAGAAATCAATGATGGGTGACGAGGAAGACAGAAA  
 TCACAAATAGGCTAAGAAGTTGAACACTATATTTATCTTGTCAGTTTATATTTAAAGAAAGATACATGTT  
 AAAAAATGTCAGGAAAGATGATCATCTAATGAAGCGAGTTACACCTCAGAAATATGATTCCAAAAAATTA  
 AAACTACATGTTTCTTTGAGTGTGGAGGATCTCTATCATCTACACATTTGTTATTTTCTTATCTCAAT  
 AAAAAACCTTAAACCAATCAAAATGATTGTTTGTATACCCACTGAATCAAGCTGATTAATTTAAAAAT  
 TGGTATATCTGAGTCTGCCAAGGTACATATGGCCATTTTAAATATACAGCTAAAAATATTTTAAATGCA  
 TTGCTGAGAAAGCTTGTCTTTCTCATCAACAGAAATAAATATTTTCAAGAGTTAA

MKALLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT  
 APSPEVSA AATISLMTDEPLDNPAYVSSAEDGQPAIS PVDSGRSNRTRARPFERSTIRSR  
 FKINRALS VLRRTKSGSAVANHADQGRESENTTAP EVFPRLYHLIPDGEITS IKINRVD  
 SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVP HNYAVRLL  
 RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDSSFHVILNKSSPEEQLGIKLVRKVDEPGV  
 FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVS RQVRQR  
 PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE  
 WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV  
 KEYEPQEDCSSPAALDSNHNMAPPSDWS PSWVMWLELPRCLYNCKDIVLRNR TAGSLGFCIV  
 GGYEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHA CLARLLKELKGRI  
 TLTIVSWPGTFL

**FIGURE 148**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCCAGGCAAATGGTGTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC  
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTTCTACCAACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGTGC  
TCTCCCGAAGAGCCTGCTTTATCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG  
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTAC  
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAAACACAT  
AATGTCGGTCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTGTTTTATCTTTTCAAAGAAATACATCC  
TTGGTTTACACTCAAAGTCAAATTAAATTCTTTCCCAATGCCCAACTAATTTTGAGATTC  
AGTCAGAAAAATATAAATGCTGTATTATA

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**FIGURE 149**

MKILVAFLLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT  
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWWKYNP  
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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MKILVAFLLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT  
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWWKYNP  
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

GGACAGAGCCAGGAAC TAGGAGGTTCTACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC  
**ATG**GGGCTCCCTGGGCTGTTCTGCTTGCCGCTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG  
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTTCCCCAAAG  
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCTCT  
 TGTGGAACCAAGACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT  
 CAACCTCAACGTCAACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT  
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
 CCAGTGTCTGAGCTGCGGGCCAACCTTACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA  
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG  
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCTGCCAACTTCTCCTTCTGCCG  
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAAGCCAATGTCCAGCACAGCGC  
 CCTCAGAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA  
 GCCCATCCTTGCTTGCCGCTCTACAGGAGCACCCGCGCTCTGAGTGAAGAGGAGTTTGGG  
 GGGTTCAGGATAGGGAATGGGGAGGTGACAGGACGCAAGCAGCAGCCATG**TAG**AATGAACC  
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA  
 GTTCATGCAAAATGAGTGTGTTTACGTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 151**

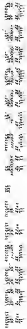
MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPGGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELRANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

### **Signal Peptide:**

amino acids 1-18

### **N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184



**FIGURE 152**

GGTCCTTA**ATGG**CAGCAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG  
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT  
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA  
 CTTTCTTCTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCCTGGGGAAGAAA  
 CTAAATGTCAACCGGCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT  
 TACAGAGCAACTGCGTGACATTCACTGAGGAATTACACACCAAGGAACCCCTCACCTGC  
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT  
 TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC  
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT  
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC  
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC  
 AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCA  
 TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACAAAAGGCTCCTGTGAGCACG  
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGT  
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCTT  
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC  
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC  
 TCTTTTGTGTTGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAATGATATT  
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCGGTGTCTTGAAAGAG  
 AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT  
 TGTTCGTACTGATATTTAAATAAAGAGTTCATTTCCCAAAAAAAAAAAAAAAAAAAAA



**FIGURE 153**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL  
HYDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS  
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81

**FIGURE 154**

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG  
CCTTGGGCCTCACAAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG  
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACCTCTGGCTGTTGATCAAAA  
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAGAAAACCTCAAATTGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC  
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT  
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGAGCAAGGGACC  
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCTGTAT  
CATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 155**

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA  
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGOPTQHFWARL

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**FIGURE 156**

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**  
 CTCTTGTGGCAGGTAAGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCTGCTA  
 CCTACGGGCCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGCCCC  
 AGAACTGCCCTCCGTTTGTCTGTCAGTAACCAAGTTCAGCAAGGTGGTGTGGACGCGCCGG  
 GGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT  
 TGGGCAGGAATCCATCCGCGAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCTCAAC  
 ACCCTGGAGCTGTTGACAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC  
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCTTCA  
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
 GAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA  
 AGACATGCCAATCTCACCCCTTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGAACCACT  
 TCCTGAGATCAGGCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCATG  
 AACTCACAGGTGAGCTGATTTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAT  
 CAACTTGGCCACATAAATCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC  
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC  
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTCCCAT  
 GCACATGCGAGGCCCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT  
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT  
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCAATGGGACAGTGCTCAGCCACGC  
 CTCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGTGCTGC  
 TTTCAGACACTGGGGTGATACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG  
 GCCTACCTCAATGTGAGCAGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT  
 AACAGTGGAGACCACGGAGATCTCGCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCTA  
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTAGACTACC  
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT  
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG  
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC  
 ACAGCCGCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC  
 AGCAGCAACAGCAGCTCCGTCCGGTGATCAGGTGAGGGGGCAGTAGTGCTGCCCAACAATTC  
 ATGACCATATTAACACAACCTACAACACAGCAGCATGGGGCCCACTGGACAGAAAAACAGC  
 CTGGGGAATCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGCCCA  
 TACCAAGGACAAGGTACAGGAACTCAAAAT**TGACT**CCCCCTCCCCAAAAAACTTATAAAAT  
 GCAATAGAAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTTGTAT  
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAGA  
 CAAAAAGTCAAAACA

**FIGURE 157**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT  
RRGLSEVPQGIPSNTRYLNLMMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNPNIESIPSYAFNRVPSLMRLDLGELKKLEY  
ISEGAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEELEMNGHNFPEIRPGSFHGLSSLKKLW  
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSSLPHDLFTPLRYLVELHLHNPWNDCDILW  
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL  
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGYYTCMVTNVAGNSN  
ASAYLNVSTAE LN TSNYSFFT VTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ  
TTRVPKQVAVPATD TDKMQTSLDEV MKTTKIIIGCFVAVTLLAAAMLIVFYKLRRHQQRS  
TVTAARTVEIIQVDEDI PAATSAAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE  
NSLGNLHPTVTTTISEPYIIQTHTKDKVQETQI

**FIGURE 158**

CGCTCGGGCACCAGCCGCGGCAAGGATGCGAGCTGGGTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCC  
 TTCTCATCTCGTCCCTTGCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGAATATCATG  
 TGTGGGAGTGTGTGAATATGATCAGATTGAGTGGCTGCGCTGCCCCGGAAGAGGGAAGTCGTGGGTATACCAT  
 CCCTTGTCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCCTGATCCACCCAGGTTGTACCATCTTTGAAAACT  
 GCAAGAGCTGCCAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCGAGAG  
 TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTT  
 GTTGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTTCATGCTAAACCTGGGTTTGTTCATCCAACATAA  
 GATTTGTTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAAC  
 CGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT  
 CCACGTCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT  
 GCTCCTCATCCCCTGTTTCCATGACGGCACGTGCGTCTTGACAGGCTGGATCTTACAAGTGTGCCCTGCTTG  
 GCAGGCTATACTGGGCGAGCGCTGTGAAAATCTCCTTGAAGAAAAGAACTGCTCAGACCCTGGGGGCCAGTCAA  
 TGGGTACCAAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTTGGCACCCTGGTGTCTT  
 TCTTTTGTAAACACTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGG  
 AAACAGCCCCATCTGCATAAAAGCCTGCCGAGAACCAAAGATTTTCAGACCTGGTGAGAAGGAGAGTTCTTCCGAT  
 GCAGGTTTCAGTCAAGGGAGACACCATACACAGCTATACTCAGCGGCTTCAGCAAGCAGAAAACCTGCAGAGTG  
 CCCCTACCAAGAAGCCAGCCCTTCCCTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG  
 TATGAGTGCATCTACCCCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAG  
 TGGGCGGGCACCCTCTGCATCCCTATCTGCGGGAATAATTGAGAACATCACTGCTCCAAGACCCAAGGTTGC  
 GCTGCGCTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCTACACAAGGGAGCGTGG  
 TTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGG  
 GAAGGTCAACATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAATTTACCGGGATGATGACCGGGATG  
 AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATCTTGCATCCCACTATGACCCCATCCTGCTTGATGCT  
 GACATCGCCATCCTGAAGCTCCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCCATCTGCCTCGCTGCCAG  
 TCGGGATCTCAGCACTTCCCTCCAGGAGTCCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGTGAGGA  
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCACTGTGGTGGACTCGCTGCTGTGTGAGGAGCAG  
 CATGAGGACCATGGCATCCAGTGAAGTGTCACTGATAACATGTCTGTGCCAGCTGGGAACCCACTGCCCTTCT  
 TGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGTCTTCCCGGGACGAGCATCTCCTGAGCCACGCT  
 GGCATCTGATGGGACTGGTCACTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTCAACCAAG  
 GTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTCTT  
 TGTATATCCGTTCTAGCTGTGTCAATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGTGCTGTGAACTTGG  
 CTGTGCCAGGGCTTCTGACTTCAGGGACAAGAACTCAGTGAAGGGTGCATTGTGCTGGTAGGCTGAT  
 GCCGGCTCCACTACTAGGACAGCCAAATTTGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAGAAAGACC  
 ATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTG  
 ACCAGGGAAGATCTGGGCTTCATGAGGCCCTTTTGGGCTCTCAAGTCTAGAGAGCTGCTGTGGGACAGCC  
 CAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTTGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCC  
 CCATCTCTGTACACATTTTAAATAAAATAAGGGTTGGCTTCTGAACACAAAAA  
 AA  
 AA

**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFFYVKG FYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLHFHSDGSKNFDGFHAIYEEITACSSSPCFHDG  
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH  
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG  
VVSVDLSLLCEEQHEDHGIPVSVTDNMFACASWEPTAPSDICTAETGGIAAVSFPGRASPEPR  
WHLMLVSWSYDKTCSHRLSTAFTKVL PFKDWIERNMK

**FIGURE 160**

ACCAGGCATTGTATCTTCAAGTTGTCTATCAAGTTTCGCAATCAGATTGGAAAAGCTCAACTTGA  
AGCTTTCTTGCCGTGCAGTGAAGCAGAGAGATAGATATTATTACCGTAATAAAAAACATGGGC  
TTCAACCTGACTTTCCACCTTTCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCTT  
GACAGTGGTTGGGTGGGCCACCAGTAACACTTCTCGTGGGTGCCATTCAAGAGATTCTCTAAAG  
CAAAGGAGTTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAAAACTCTGACT  
AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCTCTGTCTCTCTTACCTCA  
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC  
CCAAAGTGTCCAGAGGCCGTTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC  
CTCGTTCCCCACCGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAGAAAGT  
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC  
TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA  
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGT  
GATATTTTGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT  
AACAACACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGTTGAGCTCCAAAG  
AATGAAAATTTCCCGGCCCTGCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG  
ACAAGGCAATAGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG  
AGAACAGATGGGTTGAGTAGTTGTTCTTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
TATCAACATCACAGTGGATTCTTGGTTTGGTGCATGACCCCTGGATCTTTTGGTGATGTTTGG  
AAGAACTGATTCTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA  
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTCTTAGCAGAGCT  
CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG  
AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT  
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT  
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCTTTATCTCTGTACAATCATCT  
GTGAAGTGGTGGTGTCAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA  
GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGGTGCAAAGGCAG  
CAGTAGCTGAGCTGGTTGACAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT  
TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA  
TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAATAA  
TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA



**FIGURE 161**

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVYIHQAEGKKFNRAKLLNVGYLEALKEEN  
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGV TALSREQFFKVNG  
FSNNYWGWWGEGDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR  
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

**Xylose isomerase proteins:**

amino acids 191-201

GTGGGCGCGGGTTCGGCAGCGGGCTGTGGGCGCGCCCGAGGAGCGACCGCCGAGTTCTC  
GAGCTCCAGCTGATCTCCCTCCCGCTCCGCCACGCTTCTCCCGCTCCGGGCCCGCAATG  
GCCAGGACGTGTGTGTCGGCCTCGGCCGACTCTCTGGTGTGCTGCTCTCTCGCTGGG  
CCCGGCGAGGGGTGGCCGCGAGGCTGTATGAACTCAATCTCACCACCGATAGCCCTGCCACCA  
CGGGAGCGGTGGTACCATCTCGGCCAGCCTGGTGGCCACAGCAACCGGACCTTGCCCTG  
CCCGTACAGCCACCTCTACCGCTTCCACTGGATCACCAGACCCCGCTGGTGCTTATGGCAA  
GATGGAGAAAGGTTCTAGCTCCACCATCGTGTGGTGGCCACGTCGCCGGGGAATTCCCG  
TCTCTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTGT  
GTCTCTCCCATCACAGAGTTCTCTGGTGGGGACCTTGTGTGTCACCCGAACACTTCCCTACC  
CTGGCCAGCTCCTATCTCAAGACCGTCTGAAAGTCTCCTTCTCTCCACAGCCCGA  
GCAACTTGACTCAAGACCGCTTGTCTCTCACTAGCTGGGACTCTGGGGAGCCGGACCCAGATG  
GTGACTGAAGACTCCGTGGTCTATTTATAACTATTCATCTCCGAGCTTCGGGACCTTCCAGGTGAAGCT  
CAAACTGGTGGCGAGTGGGAAGAGGTGAGCGCGATGCCACAGGGCTGTGAAGCAGAAGA  
CCGGGACTTCTCCGCCCTCGCTGAAGCTGCAGGAAACCTTTCGAGGCATCCAAGTGTGGGG  
CCCACTCTAATTACAGCTTCCAAGAAGATCACGCTGACCTTGAATCTCTGGGAGCCCTCC  
TCTGACTGTGTGCTGGCGTCTCAAGCTGAGTGCTCCGCTGGAGGAAGGGAGTGCCACC  
CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTACAGGAGCCCTGGGGACTAC  
TGCTTCAGATCCGGGCCGAGAATATCATCAGCAAGACACACTAGTACCAACAAGATCCAGGT  
GTGGCCCTCAGAATCCAGCCGGCTGCTTTGCTTTCCATGTCTACACTTATCATCTGTGA  
TGTTGGGCTTCTCATGTATGACTAGCCCTCGGAATGCCACTCAGCAAAAGGACATGGTGGAG  
AACC CGGAGCCACCTCTCGGGTCAAGGTGCTGCTGCCAGATGTGCTGTGGGCTTTCTTGCT  
SGAGACTCCATCTGAGTACCTGGAATTTGTTCGTGAGAACCCGGGCTGCTCCGCCCTCT  
ATAAGTCTGTCAAACCTTACACCGTGTGACACTCCCCCTCCCCACCCCATCTCAGTGTAA  
CTGACTGTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAAGAGGGGTTTATT  
TGCTGTGGGCTGTTGGCCTGGATCCATCCATCTGTACAGTTCAGGCAGCTGCCACAAAGC  
CTCCCTCTCTGTACCCCTGACCCACGCCATCATACCATCTGTACAGTGCAGCACTGACA  
TAAGCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCTGTGAGGACT  
TTGATGCTTGGGTTGTCGTGTGACTCTAGGTGGGCTGCTGCCACACTGCCATCTCTCT  
CTCATATTGGCACAFTGCTGTCTATGGGGGTTCTCAGTTTCTCTCCCGACAGCCCTACA  
CTGTGCCAGAGAGCTAGAAAGAAGGTCTAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC  
ACATAGATGGGCACACTCAGAGAGAGAGTGTGCATGTACACACACACACACACACACA  
CACACACACAGAAATATAAACACATCGTGCATAGGCACTTCAGATGATCAGTCTGTA  
TCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA  
AGAGCCCTTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTGTCTCTGAGTTCTTG  
GCCCTTTATAGCCATCTCTGCTGCTGGCTGGCAGGGGCTGGATGGGGGCGAGGACT  
AATACTGAGTGATTCAGAGTGTCTTATAAATATCACTTATTTTATGAAACCCATCTGTG  
AACTTTTCACTGAGGAAAAGGCTTGACGCGGTGAAGAAGGTTGAGTCAAGGCCGGGCGCGG  
TGGCTACCGCTGTAAATCCAGCACTTGTGGAGGCGAGGCGGGTGGATCACGAGTACGGA  
GTGACGAGCCACCTGGCTAACACGGTGAACCCCGTCTACTAAAAAATCAAAAAAGTT  
AGCGGGGCTGGTGTGGTGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGATG  
GTGCGAAGCCGGAGGCGGAGCTTGACAGTGAGCCAGATGGCGCCACTGCACCTCCAGCGTGA  
GTGACAGCGGAGACTCTGCTCCA

**FIGURE 163**

MAQAVWSRLGRILWLACLPLWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHPGGEFPVSVWVTAADCWMCQPVARGF  
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFGDGTQ  
MVTEDSVVYYNYSIIIGTFTVKLVVAEWEVEPEPATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD  
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV  
ENFEPPSGVRCCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367



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**FIGURE 165**

MALSSQIWAACLLLLLLLLIASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCHRSKCGMCKT

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MALSSQIWAACLLLLLLLLIASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCHRSKCGMCKT

**FIGURE 166**

TGTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTCTTATAGGGAGGCAGGTGCTGGCCCTGGG  
 CTGGAATCTTCCACCATGCTCTCTCTGTGCTGCCCTTTGATAGCCGTGATTTGCAACCTCTTGGGG  
 ATCTCCCTGACTGCTCTCTTACACCTCCTTCTGCTGTTTATCATATAGTGGCCAGCATTTTTGG  
 AGTCTCCTTTGGTATCCGCAAACCTACATGAAAAGTCTGTAAAAATCTTTGCGTGGGCTA  
 CCTTGAGAATTGGAGCGAGGAGCAAGGAGAGAACCCAGCCTTTACAAGCCCTTACACCAAG  
 GGAATCATTTGCAAGGATCCCATCTTACATAGAAGAAAGATCAAGAGATCTGCTGACAGTGG  
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGC  
 GGAAGGAATGGAGACCAATTATGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG  
 GAGTCTGTGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCCGCTCA  
 GGTCTCTGTGGGGTTAGGAGTGCTGATTGCTGATCTGCTTTCTGCTGCCCTCAGGATAGCAC  
 TGGCTTTTCAGAGGATAGCCTTCTGGTGGTGGGCACAACATGTGGTGGGATACTTGCCAAAT  
 GGGAGGTTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGAATGCTGCTGCG  
 AGGCGTGACAGGCATCATCACTACCATTACAGGAAACAGACCAAGGAATGGTGGCATCT  
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC  
 ATGTTGGGTCAAAGTGACCGGGGGACATGTTGGTGTGATTCAGAGACGAGCATGGTGAAAGGCGTG  
 CCCACAGCTCTGGTTTGGCGCTCGGAAGTGAAGGATCGCCAGCTGGTGGCTAAGAGCATGA  
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATATCCTCATCTTCCCAGAAGGAACCTGCATC  
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACC  
 TGTGCTCATCAAGTATGACCTCAATTTGGCGATGCTTCTGGAACAGCAGCAAAATACGGGA  
 TGGTGACGTACCTGTGCGAATGATGACAGCAGTGGGCCATTGTCTGCAGCGTGTGGTACCTG  
 CTTCCCATGACTAGCAGAGGCAGATGAAGATGCTGTCCAGTTTGGCAATAGGGTGAATCTGCG  
 CATTTGCCAGGCAGGAGGAGCTTGTGGACCTGTGCGATGGGGGCTGAAGAGGGGAGGATG  
 TGAAGGACAGCTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCTGGGGAAACCAC  
 AAGGACAGGAGCCGTCTCTGAGCAGTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA  
 CGGGCTCAGAGCTGGAGTTGCCCGCCGCCGCCCCCATGCTGTGCTCTTTCCAGCCTCCAGG  
 CTCCTCCGGGCTGCTCTGGAATCCAGGACTCTCGGCTTTGCCGCCAGCGCAGCGGATCCTGT  
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAACCGGATGCTGCTGGGTGTTGCGACCCAGGA  
 CGAGATGCTCTGTTTCTTTTACAATAAGTCTGTGGAGAATGCCATTAAAGTGAACCTCCCA  
 CCTTTGACGCTGTGCGGGCTGAGTGGTTGGGAGATGTGGCCATGCTCTTGTGCTAGAGAT  
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG  
 CTCTCCAGGAAAGGACACAGCTGAGGACATGTGGCTGGCTTCGGCTCAACATGCCCCCAAGC  
 CTTGTGAGCTTACAGACATGATAGAGGAAGAAATGTCACTGTGAGGGCTTTACGCAAAATG  
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGGAAGAGGCCAGGTG  
 GGCGCTGATGCTGGGCCATGGGGAGAACGTGTGTTGCTATCCAGGCTAACCTTGAACCTCCC  
 ATGTGATGCGCGCTTTTGTGAATGTGCTGCTCGGTTTCCCCATCTGTAATATGAGTCGGGG  
 GAATGGTGTGATTTCTACTCATGGGCTGTGTGGGGATTAAAGTCTGCGGGTGAGTGA  
 AGGACACATCACGTTTCAAGTGTTCGAGTACAGGCCACAAAACGGGGCACGGCAGGCTGAG  
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTGTTCTGTGAGTAAATAAACTGGCTGGTGAA  
 TGA

**FIGURE 167**

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME  
RGAKEKNHQLYKPYPYTNGLIAKDPTSLEEEIKEIRRSKGSSKALDNTPEFELSDIFYFCRKGME  
TIMDDEVTKRFSAAEELESWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG  
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH  
TSPIDVIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ  
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL  
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF  
KEEQQKLYSKMIVGNHKDRSRS

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**FIGURE 168**

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCC GCCCTCACCCGGACCCCTGGCCCTCA  
CGTCTCCTCCAGGGATGCGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC  
ACCTGGCAGGCCAGGCTGTTCCACCATCCTGCCCCTGGGCTGGCTCCAGACACCTTTGA  
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC  
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT  
CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG  
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG  
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT  
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTTGGGGAGAAGAGGCGGGGCTGT  
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTGCCCCCCTG  
GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCC TGA AAGTCCA  
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
CAGCCTTGAGAAGCAAGAACATGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAGG  
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT  
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA  
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA



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**FIGURE 169**

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH  
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL  
YMRHFPFKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS  
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

**FIGURE 170**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA  
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG  
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC  
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCA  
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG  
CTCAGCAAACCTGAAGAAGATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT  
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG  
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG  
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC  
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT  
GCGTTGCCAGGAACCCCTGTGAGCAAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT  
GAAGGTGCTGCTGATGACCAGATTCCCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCCT  
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG  
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAAACTCCTAACATATGCCCCCAT  
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAAATCCTAAAGGAAGA  
TCCAGCAAATACGGTTTACTCCACTGTGAAATACCGAAAAAGATGAAAAATCCCCACTCAC  
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTTAGACAGCAGTG  
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLSKSVKQVDSIVWTFNTTFLVT  
IQPEGGTIIIVTQNRNRERVDFPDGGYSLLKSLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV  
YEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVS RNFS PILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW  
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP  
KKMENPHSLLTMPDTPRLFAYENVI

**FIGURE 172**

CTGGTTCCCCAACATGCCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
TCTGGACCCGTGAAAGAGTGGTCGGTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC  
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC  
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT  
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG  
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTATACCTGGAAGGCCCT  
GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCTCTCCCATCTCCTGGAGATGGGGAG  
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTGAGCAGAACTTCTCAAGCCCC  
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT  
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC  
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA  
ACTCCTAACATATGCCCCCATCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA  
AGATGGAAAATCCCCTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAG  
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAA**ATGA**AGATGCTGCTGCT  
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAA  
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA  
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTGATACACCCTTGACAAT  
TTTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCCTTGCACTTAA

**FIGURE 174**

MKMLLLLCGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ  
IHVLENSIVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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**FIGURE 175**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTTCATCCAGAATCCTTCAACTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG  
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC  
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTAGGTCTATGCT  
TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATGTGTAGCTTTAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTGAAAAAAAAA

MTTCCEGWTSNCGFSLVLVLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA  
IPATTMSLTARKRACNNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPNSNA  
NCEFLSKNISDIHPESFNLQWFNDSCAPPTGFNKPSTNDTMASGWRASSFHFDSEENKHLR  
IHFSVFLGLLLVGILEVLFLGLSQIVIGFLGCLCGVSKRRSQIV



**FIGURE 177**

GTGGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT  
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT  
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC  
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAAGCAAGTTGGAAGTGAAGCACTG  
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAA**TAG**TGAA  
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCAAAGTCTTTCAACGACACC  
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV  
KHCTDQISFKRRLSLKKSWWK

[illegible]

**FIGURE 179**

ATCCGTTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCGCCCACTGCCTCTCCCCTGCAGCCCTGCCCTC  
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGACACAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAAACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG  
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK  
YKSSQKQHSPVEKAIPLITPGSATTC

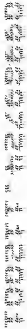
1. The first of these is the *problem of the origin of the universe*. This is a question that has been asked since the beginning of time. It is a question that has been asked in many different ways, but it is always a question about the beginning of everything.

**FIGURE 181**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCCC  
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
 CTGGCTACTCGCCCGCATCCTGGCTTGACCTATGCCCTTCTATAACAAGTGCCGCCGGCTCC  
 AGTGTTCCTCCACAGCCCCAAAACGGAAGTGGTTTGGGGTCACCTGGGCCTGATCACTCCT  
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT  
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA  
 CCAATGCCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG  
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC  
 GCGCGCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAAACA  
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG  
 CACATCAGCCTCATGACCTTGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
 TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGAGGCTCAGTGCCCTTGAGAGAAAA  
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGCGGCGC  
 TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCG  
 CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT  
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGAGAGCCATGACACCACGGCCAGTGGCCTCTC  
 CTGGGTCTGTACAACCTTGCGAGGCCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC  
 AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCC  
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG  
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC  
 TCATCGATATTATAGGGGTCCATCACAACCCAAGTGTGTGGCCGGATCCTGAGGTCTACGAC  
 CCCTTCCGCTTTGACCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTTCCTTTCTC  
 CGCAGGGCCCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGG  
 CGTTGATGTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA  
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGTGGAGCCCCGAATGTAGGCTTGCA  
 G**TGAC**TTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

**FIGURE 182**

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG  
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLF  
IRFLKPWLGEKILLSGDKWSRHRMLTPAFHFNIKSYITIFNKSANIMLDKWQHLASEGS  
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY  
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG  
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW  
DDLAQLPFLTMCVKESLRLHPPAPFISRCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW  
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT  
EPRRKLELIMRAEGLWLRVEPLNVGLQ



CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC  
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCTCTCCTTGACTCCAGGGA  
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACCTCGGAGGAGCTAGAAA  
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG  
AAAGCAGACTCAAGTACCAACATTTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT  
CTCTGGACAAGATCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAACCATACA  
AGAAACGTGAGACTCCTGATTGCTTCTGGAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT  
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC  
AGTGTGGAGAAAAACTAGGCAAACCTACACCCTGTTTATTGTTACCTGGAATAAATCCTCT  
ATGTTTTGCACAAAAAAAAAAAAAAAAA





**FIGURE 185**

GAACATTTTtagttcccaaggaatgtacatcagccccacggaagctaggccacctctgggat  
ggggttgctggtttaaaacaaacgccagtcattctatatataaggacctgacagccaccaggca  
ccacctccgccaggaactgcagggccacctgtctgcaaccagctgaggccatgccctcccc  
agggaccgtctgcagcctcctgctcctcggcattgctctggctggacttggccatggcaggct  
ccagcttcctgagccctgaacaccagagagtccagcagagaaaggagtCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTGATGTTGGAATCAAGCTGT  
CAGGGGTTcagTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA  
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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**FIGURE 186**

MPSPGTVCSELLLGLWLDLAMAGSSFLSPEHQVRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC  
GTGAACCCCGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT  
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG  
CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT  
GTCCCCCGTGTGCGCATGTGTTACAGGTGAGCCTCTCCAGAAAGTGAGATCATGGACAAAAA  
GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC  
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAATGTTCAGA  
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
CCAAAAACACAAGTAGAAATTTCTAACAATGAAATATATTACAGGCAAGGTCACCCCTAACCA  
AACAACTGAAGCGAGAGCTGTGGTCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC  
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
AACAAACAACCTCCCTGCTCCTGGCACCGAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCG  
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC  
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCTGCTCCTGACAGCTTGGCCCA  
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA  
GCATCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA  
GCCTCCTTGTTCATAACCACAGGTTACCCTACAAACCACTGTCCCACACAACCTGGGGAT  
GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA  
ATTTTTTTTAAATGAAAGTGCAATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 188

MNTWLLFLPLFPVQVQLIIVVIGIMLVLLLDFLGLVHLGQLLI FHIYLSMSPTLSPRSPQGW  
VVRAAHLTPLLEYVNPPEPPTPGARVFPVRVRCSGSASPRSEIMDKKGKSQEEIKSMRTQQ  
AQQEAEELTPRPAGVVPGA

[illegible]

**FIGURE 189**

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG  
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT  
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG  
TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG  
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA  
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG  
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA  
GGACTACTGGAATTGCCACGTTGCAAGGCCATGTACCCCACTCTCCGATTGGAGGGAA  
GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA  
TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCTCTGCT  
ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG  
CTGTTTCCTCTGTCTGTCTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC  
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG  
GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTACCACCTTCA  
ACACGTACACCAGGATGGTGTCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAAC  
CCGAAGTGCCTACCACATCACCATCAGTGTTCCTCGGCGGCTGTCAAGTGCAGCCCCCAC  
CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG  
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG  
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTTGGGGA  
GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG  
TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC  
CTAAGGGATTCTCGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC  
CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGC  
TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

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**FIGURE 190**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFGTQKVPKPLCEKGLAAKCFDMP  
VSLDGDNTNSTQEYVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFGTQKVPKPLCEKGLAAKCFDMP  
VSLDGDNTNSTQEYVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

**FIGURE 191**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCAG**ATG**TGGTTACCCCTTGGTCTCCTG  
TCTTTATGTCTTTCTCTCTTCTTCTATTCTGTCTCTCCCTCACTTAAGTCTCAGGCCTGTCA  
GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG  
TTATGGATGTTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT  
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCCAA  
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG  
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT  
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTGAG  
GACATTCGCCCCCTGTGTGCCACCAAACCAGGACTTTCCTTGGCTTGGCATCCCTGGCTCT  
CTCCTGGTACCCAGCAAGCGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTTACT  
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA  
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA  
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC  
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA  
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGG  
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG  
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC  
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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**FIGURE 192**

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGSME  
HRNHLCFCDLYDRATSPPLKCSLL

1951-52	1952-53	1953-54	1954-55	1955-56	1956-57	1957-58	1958-59	1959-60	1960-61	1961-62	1962-63	1963-64	1964-65	1965-66	1966-67	1967-68	1968-69	1969-70	1970-71	1971-72	1972-73	1973-74	1974-75	1975-76	1976-77	1977-78	1978-79	1979-80	1980-81	1981-82	1982-83	1983-84	1984-85	1985-86	1986-87	1987-88	1988-89	1989-90	1990-91	1991-92	1992-93	1993-94	1994-95	1995-96	1996-97	1997-98	1998-99	1999-00	2000-01	2001-02	2002-03	2003-04	2004-05	2005-06	2006-07	2007-08	2008-09	2009-10	2010-11	2011-12	2012-13	2013-14	2014-15	2015-16	2016-17	2017-18	2018-19	2019-20	2020-21	2021-22	2022-23	2023-24	2024-25	2025-26	2026-27	2027-28	2028-29	2029-30	2030-31	2031-32	2032-33	2033-34	2034-35	2035-36	2036-37	2037-38	2038-39	2039-40	2040-41	2041-42	2042-43	2043-44	2044-45	2045-46	2046-47	2047-48	2048-49	2049-50	2050-51	2051-52	2052-53	2053-54	2054-55	2055-56	2056-57	2057-58	2058-59	2059-60	2060-61	2061-62	2062-63	2063-64	2064-65	2065-66	2066-67	2067-68	2068-69	2069-70	2070-71	2071-72	2072-73	2073-74	2074-75	2075-76	2076-77	2077-78	2078-79	2079-80	2080-81	2081-82	2082-83	2083-84	2084-85	2085-86	2086-87	2087-88	2088-89	2089-90	2090-91	2091-92	2092-93	2093-94	2094-95	2095-96	2096-97	2097-98	2098-99	2099-00	2100-01	2101-02	2102-03	2103-04	2104-05	2105-06	2106-07	2107-08	2108-09	2109-10	2110-11	2111-12	2112-13	2113-14	2114-15	2115-16	2116-17	2117-18	2118-19	2119-20	2120-21	2121-22	2122-23	2123-24	2124-25	2125-26	2126-27	2127-28	2128-29	2129-30	2130-31	2131-32	2132-33	2133-34	2134-35	2135-36	2136-37	2137-38	2138-39	2139-40	2140-41	2141-42	2142-43	2143-44	2144-45	2145-46	2146-47	2147-48	2148-49	2149-50	2150-51	2151-52	2152-53	2153-54	2154-55	2155-56	2156-57	2157-58	2158-59	2159-60	2160-61	2161-62	2162-63	2163-64	2164-65	2165-66	2166-67	2167-68	2168-69	2169-70	2170-71	2171-72	2172-73	2173-74	2174-75	2175-76	2176-77	2177-78	2178-79	2179-80	2180-81	2181-82	2182-83	2183-84	2184-85	2185-86	2186-87	2187-88	2188-89	2189-90	2190-91	2191-92	2192-93	2193-94	2194-95	2195-96	2196-97	2197-98	2198-99	2199-00	2200-01	2201-02	2202-03	2203-04	2204-05	2205-06	2206-07	2207-08	2208-09	2209-10	2210-11	2211-12	2212-13	2213-14	2214-15	2215-16	2216-17	2217-18	2218-19	2219-20	2220-21	2221-22	2222-23	2223-24	2224-25	2225-26	2226-27	2227-28	2228-29	2229-30	2230-31	2231-32	2232-33	2233-34	2234-35	2235-36	2236-37	2237-38	2238-39	2239-40	2240-41	2241-42	2242-43	2243-44	2244-45	2245-46	2246-47	2247-48	2248-49	2249-50	2250-51	2251-52	2252-53	2253-54	2254-55	2255-56	2256-57	2257-58	2258-59	2259-60	2260-61	2261-62	2262-63	2263-64	2264-65	226
---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	-----



**FIGURE 193**

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCA  
 CGGCC**ATGGC**CAGGCATCAAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT  
 GGATGTGCCCTTCCAATATACAACAAATACTGGCCCCCTTTTGTCTATTTTTTACATCCTTTCACCTATTCC  
 ATACTGCATACGAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTTGAAGGAACCTTGCATCTTTTC  
 TTACAACGGGCATTGTGCTGTGAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGA  
 GCTTGTGCACCTTTGTTCTCACAGGAACACAGTCATCTTGCACATATACTAGGCTTTTTCTTGGTCTTTGGAAG  
 CAATGACGACTTCAGCTGGCAGCAGTGGT**GCA**AAAAAAATTACTGAATATTGTCAAATGGACTTCTCTGCATTT  
 GTTGGCCATTACGCGACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA  
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGCTGAAGGATTAAGGATTTTCT  
 CTTTTGGAAAAGCTTGACTGATTTCACACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT  
 TTATGTGTTTTCTGTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA  
 TTTGCATTGGTTAGGAATTGAGAATCCGCCGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATATT  
 TAGCCTCCATTATTACAAAAAATTATAAAATAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG  
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTCAAAATATAGCTGCATTTATACCTCAGAG  
 GGGCCAAGTGTTAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG  
 AAAATTATTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAATTTATGTTAACTTTA  
 AGGTAAGGGTGTAACAAACATTTTTGAGATAAGGTTTTTATTTATGTTTATTATGTTAGAGTGAGTTGCAATGT  
 GGGAGAATGACATTGAAATTCAGTTTTTGAATCCGTGTTCTATTTATAAGTGAATTTGTGATCTCCATC  
 AACCTTTTCATGTTTACCTTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGATGTTTGG  
 ATCATATATGCCAGAAACCTTCTCTGCTTCTCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAA  
 TAACTTTTCAAATATAGTTTAAATACACTTAGAAGTGTTACTTACCTGGAATAAATGCTATGCCGTACATT  
 CAGAGTGCCCCCTCCCCTGCAAGGCCCTGCCATGATTAAACAAGTAACTGTTAGCTTTACAGATAATTTCATGCA  
 TTAACAGTTTAAGATTTAGACCATTGGTAATAGTAGTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG  
 TATTTTAAAGCAAGTTTCTGTATACCTCTGAACCTGTTTGATTTTGAAGTTTATAGTTCATCATGATAGATCTGCTGTTT  
 CCTTATAAAAGGCATTTGTTGTGTGAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT  
 ACCTGACCAAAAAATTCAGTAACCCAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGA  
 CTTTTTTCAGGAGTGGGTATAAAAACATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTGTTTGTATG  
 TTTATTCAGTATACTTACATAAAATATTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT  
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTGAGCTTTTTTACTAAAAGATGCCTAA  
 AGCCACAGGTTTTATTGCCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAATATCG  
 GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTTTCAGATTTCAAGAGGA  
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTCTTTGCTGTGATCTACTGGACTTT  
 TTTTTTGCAGGAAGTGCATTCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTCAGTGCGAGTGCCTGCTACTG  
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTGCAATGGCAGCATT  
 GTGCTCTTGACATCTGTATAGCTTGACATAGTGCTGTCTGATTCTAGGCTAGTTACTTGAGATATGAAT  
 TTTCATAGAAATATGCATGATACAACATTACCATCTTCTATGAAAGAAACCTTTTGATGATGAACAATAA  
 AGATTTTAAATATCTATTTTAAAAA

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**FIGURE 194**

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLEVLFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND  
DFSWQQW

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MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLEVLFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND  
DFSWQQW



**FIGURE 196**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH  
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ  
ITQLPNTTFRMPENLRSVDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV  
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRPTYIEPRIILNSWKSLSIT  
LAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASEPYAQGEDVLDVYAFHLCEDGAEPTSG  
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVGTMA  
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH  
IEGALVIINEYGSCTCHQQPARECEV

**FIGURE 197**

GTGCAAGGAGCCGAGGCCGAGATGGGCGTCCTGGGCCGGGTCTCTGTGTGGCTGCAGCTCTGC  
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGCGAGCCAA  
CTGGAGCCAGAACCGGACCCCCGTGCGCCGGCGCGCCGTTGAGTTCCCGGCGGACAAGATGG  
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA  
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG  
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT  
GGCGCTCTGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC  
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG  
CCCCGTGCGTGTCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG  
CTGTTTTCTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTTGAGCGTG  
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG  
GATCTGCGCGGCCCTGCTCCAGCCCCCT





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**FIGURE 200**

MGPVKQLKRMFEPTRLIATIMVLLCFALTICSAFWWHNKGLALIFCILQSLALTWYSLSFIP  
FARDAVKKCFVCLA

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**FIGURE 201**

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGGCGTTCCCTCCAGTCACCCCTCCGCGCGTTACCCGCGGCGCGC  
 CCGAGGGGAGTCTCCTCCAGACCCCTCCCTCCCGTGTCTCCAACTAATACGCACTGAACGGATCGCTGCGAGGGT  
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCCATCCATAGCCAGATAGATTATCTTACACTG  
 AACTGATCAAGTACTTTGAAATATGACTTCGAAATTTATCTTGGTGTCTTCATACCTGCTGCACTGAGTCTTTC  
 AACCACTTTTCTCTCAACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACT  
 TATATAAAGTTCCAACGCCCATTTTCATTATATTATGAATATGGTGTACAGTGAAGCAAGTTACTAAATGTT  
 TTTATTACAAAACCTACCCTAACCATTTATACCTTTGGTAACTGGCTCTTTGAGAGAATCATGGGATTGTTGC  
 AAATGATATGTTTGATCCTATTTCGGAACAAATCTTTCTCCTTGGATCACATGAATATTTATGATCCAGTTTT  
 GGGAGAGGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA  
 ACAGATGTAAAAATACATAAGCGCTTCTTCTACTCATACATGCCTTACAATGAGTCAGTTTCATTGGAAGATAG  
 AGTTGCCAAATGTTGAATGGTTTACGTCAAAGAGGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCGTG  
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCTGTCTTTGAGATATTGACAAGAAGTTA  
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAGTGATCATGG  
 AATGACGCGAGTGTCTGAGGAAAGGTTAATAGAACTGACCAGTACCTGGATAAAGACCACATATACCCTGATTG  
 ATCAATCTCCAGTAGAGCCATCTTGCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT  
 CATCCTAATCTTACTGTTTACAAAAAGAGAGCGTTCAGAAAGGTGGCATTACAAATACAAACAGTCCGAATCA  
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCACATTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC  
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCGCTTCAAGAAAGATTTTC  
 TCAAAAGAAGCCATGAACCTCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA  
 CAATGGATCATCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA  
 CTATACTCCTCCCTGGTAGTGTTAAACAGCAGAATATGACCAAGAGGGGTATACCCCTTATTTTCATAGGGGTG  
 TCTCTTGGCAGCATTATAGTGATTGATTTTTTTGTAATTTTCATTAAGCAATTAATTCACAGTCAAAATACCTGC  
 TTTACAAGATATGCATGCTGAAATAGCTCAACCATTTATTACAAGCCTAATGTTACTTTGAAGTGGATTGCTATA  
 TTGAAGTGGAGATTCCATAATTATGTAGTGTTTAAAGGTTTCAAATTTCTGGGAACCCAGTTCCAAACATCTGC  
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACACCGACCAA  
 ATACTTACACCTGCAAAGGAATAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG  
 ATCCTGCTTTATTTGGACTTGGCGAGATAATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTTATAT  
 ATTGCACTTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAAC  
 TTGATTGAAATGACAACTTTTTCACCCATGTACAGAATACTTGTTCAGCATTGTTCAAACCTGAAGGAAATTT  
 TCTAATAATCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGGTGATAAGTGTGTA  
 AATTTAAATGTATAACCTTTGAACCTTGAATTTTGAGATGTATTTCCCAACAGCAGAATGCAACTGTGGGCAT  
 TTCTTGCTTATTTCTTTCCAGAGAAGTGGTGTTCATTATTTTCCCTCAAAGAGAGTCAAACTAGTACAG  
 ATTCGTTCTAAATATATTGTTTCTGTATATAAATATTGTGATTTCCTGATGAGTCATATTACTGTGATTTTCA  
 TAATAATGAAGACCCATGAATATATTTTCTTCTATATAGTTACAGCAATGGCTGAATAGAAGCAACCCAGGCA  
 CCATCTCAGCAATGTTTCTCTTGTGTAATTTATTTGCTCCTTTGAAATTAATCACTATTAATTACATTAA  
 AATCAAATTTGGATAAAAAAAAAAAAAAAAAA

**FIGURE 202**

MTSKFILVSFILAALSLSTTFSLQLDQKVLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRINKSFSLDHMNIYDSKFWEEATPIW  
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY  
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER  
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN  
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD  
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF  
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 203**

GGATTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCCAG  
GACAGGCCCACCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC  
AGAGAGGCCAAGCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAATCACAA  
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC  
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA  
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG  
AGCAGCCACCACCACACCAAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCC  
CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT  
CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC  
TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG  
GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT  
ATTTGTCTTCCGCCTGAGTTCTTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG  
TGGTCTCATTCATCCTGGACATTTGCCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC  
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT  
TAAGACACGTTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA  
AGATTCAACACCTTGAGTTCAGTGCTCTGAGAAGCCCCTGACTGATGAGTTTGCTGTATC  
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT  
CACACAGCCACCCTGAAAGTCTTGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG  
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA  
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC  
AAAAATCTATAAAGATATTTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDDYHAWNINYYKKWENEEEEEEQQPPTPV  
SGEEGRAAAPDVAPAPGPAPRAPLDFRGLRLKLFSSSHRFQVIIICLVVLDAALLVLAELILDL  
KIIQPDKNYYAAMVFHYMSITILVFMMEEIIFKLFVFRLSSTTSLRSMWPVVVVVSFILDI  
VLLFQEQHFQALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS  
CSEKPLD

**FIGURE 205**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAACAT  
 GCTCTGTCTGTGCTGTACGTGCCGGTCACTCGGGGAAGCCAGACCGAGTTCACAGTACTTTG  
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC  
 CAGGAATTTCTCCACCTACCGCCAGTGGAAAGCAGAAAAATTTCAAGCTGGAGATAAGGACCT  
 TGATGGGCGAGCTAGACTTTTGAGAAATTTGTCCATTATCTCAAGATCATGAGAAGAGCTGA  
 GGCTGGTGTTTAAGATTTTGGACAAAAAGAAATGATGGACGATTGACGCGCAGGAGATCATG  
 CAGTCCCTCGGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCAAGAG  
 CATGGATAAAAAACGGCAGATGACCATGACCATGGAACGAGTGGAGAGACTACCACCTCTCC  
 ACCCGTGGAAAAACATCCCGGAGATCATCTCTACTGGAAGCATTCACGATCTTTTGATGTG  
 GGTGAGAACTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTG  
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACTGACGCGCCCCCTGG  
 ACAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAATGGGCATCGTTGGT  
 GGCTTCACTCAGATGATTCGAGAAAGGAGGGGCCAGGTCCTCTGGCGGGCAATGGCATCAA  
 CGTCTCCAAATTTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC  
 TTGTTGGTAGTGACCAGGAGACTCTGAGGATTACAGAGGGCTTGTGGCAGGGTCTCTGGCA  
 GGGGCCATCGCCAGAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCGCTCGG  
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTCGCCAGGAGGATCTGGCCAGAGAGGGGG  
 TGGCCGCTTACAAAAGGCTATGTCCCCAACATGCTGGGCATCATCCCTATGCCGGCATC  
 GACCTTGCAGTCTACGAGACGCTCAAGAATGCCGTGGCTGCAGCATATGCAGTGAACAGCGC  
 GGACCCCGGGCTGTTTTGTCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG  
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCTCTATTGAGGCGCT  
 CCGGAGGTGACCATGAGCAGCCTCTTCAAACATATCCTCGGACCCAGGGGGCCTTCGGGCT  
 GTACAGGGGCTGGCCCCAACTTCATGAAGGTATCCAGCTGTGAGCATCAGTACGTGGT  
 TCTACGAGAACCTGAAGATCACCTGGGGCTGCAGTCCGGGTCAGCGGGGAGGGCCGCCG  
 GCAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATG  
 TGCCAAACATAAGCTGTCTCGAGCCAAAGCTGTGAAAACCTCAGACGCCCCCGCAGGAGGGT  
 GGGGAGAGCTGGCAGGCCCAGGGCTTGTCTGTGACCCAGCAGACCCCTCTGTTGGTTCC  
 AGCGAAGACCACAGGCATTCCCTAGGGTCCAGGGTCAGCAGGCTCCGGGCTCACATGTGTAA  
 GGACAGGACATTTTCTCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCGGGCTTAGT  
 TCTTCCATTTCACCCTTGCAAGCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGC  
 ATCTCCTCTGTGCCCTCTTGTCTGCCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAG  
 CCCACATCCCACCCCTCGTCCAATCCATAATCCATGATGAAAGGTGAGGTACAGTGGCTCC  
 CCCAGGCTGACTTCCCAACGTACAGCATTGACGCCAATCTGGCTGTGAAGGAAGAGAAAG  
 GATCTGGCCTTGTGGTCACTGGGCATCTGAGCCCTCTGATGGCTGGGGCTCTCGGGCATGCT  
 TGGGAGTGCAGGGGGCTCGGGCTGCCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCA  
 TGGTGTCTGAGCTGGCCTGGACCCTGTCAAGGATGGGCCCCACCTCAGAAACCAACTCACTG  
 TCCCCACTGTGGCATGAGGGCAGTGGAGCACCATGTTTGAGGGCGAAGGGCAGAGCGTTTGT  
 GTGTTCTGGGAGGGGAAGGAAAAGGTGTTGGAGGCCCTTAATATGGAATGTTGGGAAAAGGG  
 TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGCAGGG  
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTGCCAAC  
 CCAGCAGGGGCGCAGCGGCCACCCACATTCACATTTGTGTCACTGCTTGGAACTTATTT  
 ATTTTGTATTTATTATTAAGACAGATTATGTCCAACTATTTTATAGATTGTGTTAATTAATA  
 GCTTGTCAATTTCAAGTTTCATTTTATTCATATTTATGTTTCATGGTTGATTGTACCTCCC  
 AAGCCCCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGCCCTTGGCCAGCTGCAGTACAT  
 CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAGGCGAGCAGCCCTG  
 GCTCCTTTCTTTGGCAGGTTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTCAGGTTTGA  
 CTGGGGGCGTGGAGAGAGAGGAGGAGAACCTCAATAACCTTGAAGGTGGAATCCAGTTATTTT  
 CTGGTGTCAAGGGTTTCTTTTCTTCTTCTTCTTCTGATGTCAAGGCGAGGTGAGGTGCTCT  
 CACTGTGAATTTGTGGTGGGCGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCGCTCCCTCC  
 CAGCCTTCTGCTGCCCTTGTCTTAAACAATGCCGGCCAACTGGCGACCTCACGGTTGCACTTCC  
 ATTCACCAAGAACTGATGAGGAAATCTCAATAGGATGCAAGAGATCAATGCAAAAAAT  
 GTTATATATGAACATAAATCGGAGTCGTCAAAAAGCAAAATTAAGAAAGAAATGGACGTTAG  
 AAGTTGTCAATTTAAAGCAGCCTTCAATAAAGTTGTTTCAAAGCTGAAAAAAGAAAAA  
 AA

**FIGURE 206**

MLCLCLYVPVIGEAOQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD  
LDGQLDFEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK  
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMW  
WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI  
NVLKIAPESAIFKEMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIIYPMEVLKTRMAL  
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS  
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSSLFKHILRTEGAFG  
LYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation site.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

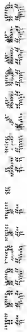
amino acids 54-73, 85-104, 121-140

**FIGURE 207**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**  
**GG**CTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG  
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC  
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACTGACATCAA  
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA  
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGTTT  
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC  
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA  
 AAACCTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG  
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA  
 GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAAATGTGACCA  
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACCTCTGTATGATTGAA  
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG  
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGCTCTCTCTTTCTTTGCCATCAGCT  
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAG  
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG  
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA  
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA  
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGTGATAAG  
 TAAAATGCACGTGGAGACAAGTGCATCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCTT  
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG  
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA  
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG  
 GCGGCTGCATTTTAGTAATGGGTCAAATGATCACTTTTTATGATGCTTCCAAGGTGCCT  
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA  
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA  
 AA

**FIGURE 208**

MASLGQILFWSIISIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRТАVFADQVIVGNASRLKNVQLTD  
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTSEIKRR  
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK





[illegible]

210/330

**FIGURE 210**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQC  
GSLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSS  
FPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVFPFPWTVWRKTEAGVWD

210/330  
MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQC  
GSLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSS  
FPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVFPFPWTVWRKTEAGVWD

**FIGURE 211**

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT  
 TTGCCAGTGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG  
 TTGCTGGTATCACTGCAGTGCTTGTGGCAGCTGTAGAATCTCTGAGCTGCCGTGCAGTGTAAT  
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCCTCTGAATGTCCCTCACATGCCAACACCAG  
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT  
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT  
 GCTGAAGAACACTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG  
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG  
 AATCTAATGGAACCTTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTTGTC  
 TTTCTAGTTGCAGAACCTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT  
 CAACGTCAGTAACGCCACCTGTGAGTTCCCTGTCTGGTGAAAACAAGACTCTTGAGGAGTCA  
 TCTTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT  
 TCCCACAACGTGGGCTCCAAGCTTCCCTCTACCTCTTGCCCTTGCCAGCCTCCTTCTTCG  
 GGGACTGCTGCCTGAAGGTCTGGGGCTGCACCTTGCCAGCACCCCATTTCTGCTTCTCTG  
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC  
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA  
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 213**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA  
GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCAGCCCC**ATG**GTCCCCGCCGCCG  
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCCTG  
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGGCCCATGACCCGCAG  
CTACCGGAGCACGCGCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
ATGATGCCATGGCCGACGCCACCGCCTGGCTGGACAGCGGCTGCCGAGCTCTTGCCGCC  
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTACGAGGAGGATGGGTCTTCAGAAGA  
GGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA  
ATACAGCGGGGAGTTCCAGCACGAGGTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
ACTTCAAGCCTGCCCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTACCCACAG  
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTCTGATGCCCTGGGGCCCGTGGCACTGCCAC  
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCCTTCCGGGCGCCT  
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC  
CCTGCAACCGACTTCGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT  
GCCTCTCAGAGCACCACAGTACCAGGACCACCTACCCCTTCCCCACCATCCACCTCAG  
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA  
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTCAGTGTTACAGAGATGCAACCAATA  
GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT  
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTACAGAAAAACAAAACCTGGAAAA  
CACAA

**FIGURE 214**

MVPAAGALLWVLLLNLGPRAGAQLTQTPTEMQRVSLRFGGPMTRSyrSTARTGLPRKTRI  
ILEDENDAMADADRLAGPAAAEELLAATVSTGFSRSSAINEDGSSEGVVINAGKDSTSREL  
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP  
SPSPTAMPSPEDLRLVLMFPGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC  
TYQQCPNRLREECPLDTSLCDTDNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA  
FWKRVRIGLEDIWNLSLSSVFTEMQPIDRNQR

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**FIGURE 215**

CCGGGGTCGACCCACGCGTCCGGGGAGAAAGCATGCGCGGCTGGCGGCGGGTGGTCTGCTAGCTGGGGCA  
 GCGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGGTGTACCGGAGCTGCGTACTGCAGTGCGAAGAGCA  
 GAACTGCTCTGGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT  
 CTGCGGGACGACTGTAAGTATGAGTGTATGTGGGTCAACGCTTGGGCTCTACCTCCAGGAAGTGCACAAAGTGCCT  
 CAGTTCATGGCAAGTGGCCCTTCTCCGGGTTCTGTCTTTCAAGAGCCGGCATCGGCCGTGGCCCTCGTTTCT  
 CAATGGCTGGCCAGCTGCTGATGCTCTGCCGCTACCGCACTTCTGTGCCAGCTCTCTCCCATGTACACCA  
 CCTGTGTGGCCTTGCCTGGGTGTCCTCAATGCATGGTCTGGTCCACAGTCTTCCACACCAGGACACTGAC  
 CTCACAGAGAAAAATGGACTACTTCTGTGCCTCCACTGTCTATCTACACTCAATCTACCTGTGCTGCGTCAGGAC  
 CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGACGTCT  
 CTTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGCCAACGTGGCTATTGGCCTGGTCAACGTG  
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACAGCGCGCGCTGCCTCACGTGCGCAAGTGCCTGGTGGTGGTCTT  
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTTGGATGCCCATGCCA  
 TCTGGCATCAGCACCATCCCTGTCCACGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG  
 AAGGAATCAGAGGACAAAGTTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC  
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCCCTGAGATGATTTTCTCTTTTCAACTTCTTGAAGTGGACATGA  
 AGGATGTGGGCCAGAATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTCTAGGG  
 AAGCCTCCCAGCATCTGGACTCGAGAGTGGGACGCCCTCTACCTCTCGAGCTGAAGTGGGGTGGAACTGA  
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTTCTCTCCACAGCCTCTCTCCACATCCCCAGCTG  
 CCTGGCTGGTCTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGACACAGGCCTTAGGGATACAGGGGGTCC  
 CTTCTGTATCCACCCCCACCCCTCCTCCAGGACACCACTAGTGGTGGTGGATGCTTGTCTTTGGCCAGCCAA  
 GGTTCACGGCGATTCTCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC  
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCA  
 AGGATCCTGTGCTGCTGTCTGGTTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGCCAGGCTGAGTGCATAGG  
 TGACAGGCGCGTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCCTAGTGTGCGAGTGTGGAGACGGGTGTTGT  
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGAGGGGGTGGTGTGTGAGCTGGGTAGGGGAACGTGTG  
 TGCGCGTGTGCTGGTGGGCATGTGAGATGAGTACTGCCGCTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT  
 GAGGGAATCCTGTCAACATCAATAACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGCGGACAGC  
 CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGGTGCCCCCTTGTCCGCCCTCTGCAAAAC  
 CTCACAGGGTCCCAACACAGTGCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAATGGGGATGGC  
 TGGGGCTCTCTCCATCTCCTTTTCTCCTTGCCTTCGCATGGCTGGCCTTCCCTTCCAAACCTCCATTCCCT  
 GCTGCCAGCCCTTTGCCATAGCCTGATTTTGGGGAGGAGGAAGGGGCGATTGAGGGAGAAGGGGAGAAAGCT  
 TATGCTGGGTCTGGTTTCTTCCCTTCCAGAGGCTCTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCC  
 ACACATATGCCTGTGCCCTGGTAAAGGAGTGCCTTGCATTTACACAGCAGCCCTGGCATGTCTCTGCCCCACAGG  
 AATAGAAATGGAGGAGCTCCAGAACTTTCCATCCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGT  
 CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGACTCGGGT  
 GCCTGCGCTAGCTTCTTTTATCTGAAACTTTTAAAGTGGGAGGTGGCAAGGATGTGCTTAAATAATCAA  
 TTCCAAGCTCAAAAAAAAAAAAAAAAAA

**FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
TCRDDCKYECMWVTGGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFNLGLASLVMLCR  
YRTFVPASSPMYHTCVAFAVWSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR  
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWVWLAWCLWNQR  
RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL  
KESEDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186



[illegible]

**FIGURE 218**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEHEEL  
 DAEVLEVVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLOYEDKFRNNLKGKRLDINTN  
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV  
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF  
 VLGAAFSSNPVKQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
 GGLQVLRTLVQEKGTAVLAVRVVTLTYDLVTEKMFABEEAEELTQEMSPEKLQQYRQVHLLPG  
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCDRDYRQDPQLGRTLASLQAEYQVLAS  
 LEIQDGEDEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340



**FIGURE 219**

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCC  
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGCGTTGCCACCCCA  
 CGCGGACTCCCCAGCTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCCACCCTCC  
 TTCCCACTGACCAGGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTTCGGC  
 CCGGCCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGT  
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTTCATCTTGG  
 TCCATGTGACCGACCGGTACAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT  
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA  
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT  
 ATGTTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGCTTCTCTGTTATCAATATTTGGCT  
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCCATTACTTCTCTGACTTC  
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG  
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCCTGGTGGTTGGGAGTCACCTACTGACATCG  
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT  
 TTCCATGGGGCTCTGGGCCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC  
 TCTTGTGTAAGGACTTGACTACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG  
 CCCATGACTGAGCCCAGCCCCAGCCCGGGTCCATTGCCACATTCTGTCTCCTTCTCGTC  
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT  
 TACCAGGAGCAGCCTGGGTTACGCCAGTCAGTGACTGGTGGGTTTGAATCTGCACTTATCCC  
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTAGTGCTCTGCTCTCAC  
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGACGGCCGACGGCAGGAGGACAGTCGGGTGAT  
 GGTGTATTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC  
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTCTCCATCTCCAGTCTTGGACAGTGCAG  
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA  
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC  
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCCTAAACTGCCTTTTTTCTTTTTT  
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTAACCTCCTTGGGCTATATTTTCTC  
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCAGACCTT  
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAAGTGGCATTACTGGAATAATGGTTTTAACCT  
 CCTTAACCACAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGC  
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG  
 GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGT  
 ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT  
 AATAAAAAAGAAATTTGTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 220**

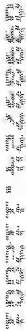
MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR  
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEdGRSPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVGIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR  
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR  
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEdGRSPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVGIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR  
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

AAGCTGGTTTAAAGGAAGCAGAGGAGGGTTAGATTCTGTTGAGTGAGGACGGAAGATCAACCCA  
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT  
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTGGGATCCATGGAGAC  
TCACCCATTANTTCTGANTTACGCCTTTNTGACAGCAGCCATTATCCTGCCTC

**FIGURE 222**

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG  
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN  
TGGINTTTCCTTCGGTATCATCAGTGGTGTNTCTGTATCAATATTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAATTCCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGGATGCCTGTGA  
GAGGAG



**FIGURE 223**

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCCG  
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCTTCCACNTG  
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTGCGCCCGGCCTTCG  
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC  
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTGTCC  
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG  
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATTCAATATTTGGCTGATGCACTTG  
GGCCAGGTGTGGTTGGGATCCATGGAGACTACCC

**FIGURE 224**

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCCNNTCCCCGGG  
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC  
CAGNTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTGCGGCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC  
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA  
CCGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGCTCTGTG  
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGTT  
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTGGCTGATGCACTT  
GGGCCAGGTGTGGTTGGGATCCATGGAGAC



**FIGURE 225**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG  
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC  
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAG  
 TGTCTGTGCGTCTGCAACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGT  
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGCCCGT  
 CCTTGTGGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC  
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT  
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA  
 GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA  
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC  
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGTGCTCACGGCCGCCCACTGTCAG  
 GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC  
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT  
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTTCGTCCCACTAAAGATGTAGACCCAT  
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGCTGGCTGGGGGACAA  
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT  
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA  
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC  
 TGCAGGGACTCGTGTCTTGGGGAGATTACCCTTGTGCCCGGCCAACAGACCGGTGTCTAC  
 ACGAACCTCTGCAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTTGAGTCAT  
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG  
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT  
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCCTGG  
 GAACAATTTCCAAAACCTGTCCAGGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCAT  
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA  
 CTGAGAAGTGGAATAAAAAA

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**FIGURE 226**

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD  
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PYYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL  
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSSGP  
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PYYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL  
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSSGP  
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

**FIGURE 227**

**ATG**GTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCGCGCGGA  
 CAAGCCGACGCGGCGAGCTGCGGGCTACGTGCTGTGCACCGTGCTGCTGCCCTGGCTGTGTC  
 TGCTGGCTGTAGCTGTCAACGGTGGCGGTGCTCTTCCCTGAACACGCGCCACGCGCGGCGACG  
 GCGCCCCACCTGTGCTGACACTGGGGCTGCCAGCGCCAAACAGCGCCCTGGTCACTGTGGA  
 AAGGGCGGACAGCTCGACCTCAGCATCCTCATTGACCGCGCTGCCCCGACCTCACCAGCA  
 GCTTCGACGCGCTGGAGAGCGCCAGGCGCTCGGTGCTGCAGGCGCTGACAGAGCACCAGGCC  
 CAGCCACGGCTGGTGGGCGACACAGGAGCAGGAGCTGCTGGACACGCTGCCCGACCACTGCC  
 CCGGCTGCTGGCGGACGCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG  
 GCACGCTGGGGCAGGGCCCTCAGCGCCCTGCAGAGTGAGCAGGGCGCGCTCATCCAGCTTCTC  
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTGACGGACATCCTGGATGCCCT  
 GCAGAGGGACCGGGGGCTGGGGCGGCCCCGCAACAAGGCGGACCTTCAGAGAGCGCTGCC  
 GGGGAACCGGCGCCCGGGGCTGTGCCACTGGCTCCCGGCCCCGAGACTGTCTGGACGTCTCT  
 CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTTCCACCCACTACCGGCGCGGCTT  
 CCAGGTGTACTGTGACATGCGCAGGACGGCGGCGGCTGACGGTGTTCAGCGCCGGGAGG  
 ACGGCTCCGTGAACCTTCTTCGGGGCTGGGACGGTACCGAGACGGCTTTGGCAGGCTCACC  
 GGGGAGCAGTGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGT  
 GCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCCCTATGCCCGCTACGGGAGCTTCGGCG  
 TGGGCTTGTCTCCGTGGACCTTGAGGAAGACGGGTACCGCTCAGCGTGCTGACTATTCTG  
 GGCACCTGCAGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTACCACCAAGGACCTGGA  
 CGCGACCATTCAGAGAACAACCTGTGCCGCTTCTACCGCGGTGCTGGTGGTACCGCACT  
 GCCACAGCTCCAACCTCAATGGCGAGTACCTGCGCGGTGCGCAGCGCTCCTATGCCGACGGC  
 GTGGAGTGGTCTCTGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG  
 GCCGCTCCGGGAGGACCG**TAG**ACTGGTGCACCTGTCTTGGCCCTGCTGGTCCCTGTGCG  
 CCCATCCCCGACCCACCTCACTCTTTCCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC  
 CCACTCTCCAGTAGGGAGGGGCGCGGCCATCCCTGACACGAAGCTCCCTGGGCGGTGAAGT  
 CACACATCGCCTTCTCGCGCTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCTC  
 TGCTGATGGGGGCTGGCAAACCTTGACGACCCCAACTCCTGCCTGCCCCCACTGTGACTCCGG  
 TGCTGTTTGCCGTCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGCACCTCTGCCCTGCC  
 GGCCAAATACCGGCATTATGGGGACAGAGAGCAGGGGGGAGACAGCACCCCTGGAGTCTC  
 CTAGCAGATCGTGGGGAATGTCAAGTCTCTCTGAGGTCAAGTCTGAGGCCAGTATCTCCAG  
 CCTCCCAATGCCAACCCCAACCCGCTTTCCCTGGTGCCACAGAAACCCACCTCTCCCCAA  
 GGGCTCAGCCTGGCTGTGGCTGGGTGGCCCATCCTACAGGGCTGAGGTCAAGGTCAAGATGG  
 GAGCTGTGCTTGTGGGAGCCACGCTCCAAGGCTGAGACAGTTCCTTGGAGGCCACCCAC  
 CCGTGTGCCCGGCGAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCCTCACTGCTCTG  
 TCTCAAATGAGGCCCAACCCATCCCAACCCAGCTCCCGGCGCTCCCTACCTGGGGCAGC  
 CGGGGCTGCCATCCATTCTCTCTGCCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT  
 GGACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCTAGGCAGGGCTGGGATGAG  
 GCTTGTACAACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCTCCAGGAGG  
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTGCC  
 ATTGACCGTGGCCACTGGACCCAGGCCAGGCCCGCGCCGGCGAGTGGTCAAGGGACAGGGA  
 CCACCTCAGCGGCAATGGGTGGGGGAGCTGGGGCACCAGACAGGACACCACTGGACA  
 CTTTCTTGTGAATCTCCCAACCCAGCACGCTGTCTATCCCACTCCTTGTGTGCACACA  
 TGCAGAGGTGAGACCCGAGGCTCCAGGACAGCAGCCACAAGGGCAGGGCTGGAGCGGG  
 TCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCTGCGTTACGTCAAGGCCAGATGCCAGG  
 CGGCTTTTCCAAAGGCTCTCTGATGGGGGCTCCGAAAGGGCTGGAGTCAAGCTTGGGGAGCT  
 GCCTAGCAGCCTCTCTCCGGGACGAGGGGAGGTGGCTTCTCCAAAGGACCCGATGGCA  
 GGTGCTTAGGGGTGTGGGGTTCGGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA  
 AACATAAATTTGACCTGGCACCACTGGGGGTGTGGGAGAGGCCGTGTGACCTGGCTCTC  
 TGTCCAGTGCCACCAGGTCATCCACATGCGCAG



**FIGURE 229**

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT  
 TGCTTCTCGAAGTAGCTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT  
 CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG  
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAAC**T**CGGCATCCAGAGCCC  
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCC**T**GCTGAC  
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGT**TTTTT**TCAGTACTACC  
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC  
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGAGTCTGCAGCATGTGGC  
 TGA**AAAA**CTCTGTGCTGAGCTGTATAACAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
 AACAATGGAATGGCATGGAGACAATTGTCTACAGTTCTATAAAGACAGCAAAAGTTGGGAG  
 GACTGTAAATATTTCTGCCTTAGTGAAA**ACT**CTACCATGCTGAAGATAAA**CA**AGAAGA  
 CCTGGAA**TTT**GCCCGCTCTCAGAGCTACTCTGAGTT**TTTT**CTACTCTTATTGGACAGGGCTTT  
 TGGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG  
 TTCCATATTATAATAGATGTCACCAGCCC**A**GAAGCAGAGACTGTGTGGCCATCCTCAATGG  
 GATGATCTTCTCAAAGACTGCAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA  
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGCGAAGGTGAC**TGA**TTCGCC  
 CTCTGCAACTACAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT  
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAATGGGTTCTCGTG  
 TTTCTGTTCAGGATCACCAGCATT**T**CTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA  
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG  
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT  
 GTCTTCCTTACACTGGTGGAATAAGAA**ACT**TTTTGAAGTAGAGGAATACATTGAGGTAA**C**  
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACC  
 AGCAAATACACAAGGAATTTCTTTTGT**TTT**TCAGTTCATACTAGTCCCTTCCCAATCCAT  
 CAGTAAAGACCC**ACT**CTGCCTTGTCATGCCGTTTCCCAACAGGGATGCACTTGATATGAG  
 AATCTCAAATCTCAATGCCTTATAAGCATTCTCTGTGTCCATTAGACTCTGATAATTG  
 TCTCCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTT**CAT**ATCAG  
 AACTACCGTCCCGATATTTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA  
 TCTGCACCTGTAATAGTTTCAGTTCTATTTTCTTCATTGACCCATATTTATACCTTT**CAG**  
 GTACTGAAGATT**TAATAATAATAA**TGTAATACTGTGAAAAA

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**FIGURE 230**

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCVLVLL  
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE  
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS  
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD  
CKELKRCVCERRAGMVKPESLHVPPETLGEGD







**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP  
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVTRYISTELGIRQLLVAVL  
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE  
QHGDDEFWFFLVPDTTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAEELERTYQEIQELQWEIQNTSHLAVDGDRA  
AAWPVGIPAPSRPASRFEVLRWDFTEQHAFSCADGSPRCPLRGADRADVADVLTALEELN  
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL  
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPELGRDTGRFDRQAASEACFYNS  
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL  
YHRCLQSVLEGLGSRTQLAMLLEQEQQNST

**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT  
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCTTTGAAGATGAAAG  
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
 CTGTATCCACCCAAATGTCACCGATTTCTTCTTATGCAGGAAATGAGCAGACCCATCAATAA  
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAG  
 AGGGTTGCTCAACGCCCCGCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG  
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC  
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCGCGTCCGCTGGGA  
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCCAGAAC  
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCA  
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGTCTGGAACATGCGACTTGCTTCTT  
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**  
**ACC**AGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC  
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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**FIGURE 235**

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE  
DENLYEKNPDSHGDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPEDE

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MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE  
DENLYEKNPDSHGDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPEDE

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAAGCGGCCCCAGAACCGACCACACCGTGGAAGAGGACCCAGAACCCGAGGA  
CGAAACTTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG  
TCTGGAACATGCGACTTGCTTCTTCTTTGGCGCTCCATCATCTGGTCCTTGGCAGCAC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACTGCTTCGACCCAGCA  
AGATCCAG

**FIGURE 237**

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGCTCCTGGGGCCCCGGCGGCTGGTGCCT  
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTCAATACCCCCGCTGCCTTCCGGGG  
 ACGTAGCCGCCACATTCAGTTCCGACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTG  
 TCCCATTACAGGCTCTTTCCCAAAGCCCCGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA  
 GCTGCACCTGTCAATCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTCCTGC  
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA  
 TCTTGAAGGAGCTCAGTAATGCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA  
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG  
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC  
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA  
 TCGCTTTGTTCCACACCAGTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG  
 CACGCTGTAAGTACATCTCCTGGGAGCTGAGGCAGACCCGTGTAGTTGATTTGATGCCTTC  
 ATCAGGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA  
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACACCTACAACCAGGACA  
 ACGAGACATTAGAGGTGACCCACCCCGACCACTACATATCAGGACGTCATCCTAGGCACT  
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACTCTCGAAACCT  
 CAACATCCAGCTCAAGTGAAGAGACCCCAAGAGAATGAGGCCCCCCCAGTGCCCTTCTGC  
 ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC  
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGTGCTGGACACCGTACCTGGTATCTGCG  
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC  
 ACTACCAGCCTGCCCCAGGACCCGGCTGCAACCCACCTCCTGGAGATGCTGATTAGCTGCCG  
 GCCAACTCAGTCAACCAAGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA  
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCTTGTGCCCCA  
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA  
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC  
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT  
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGACAGGT  
 GGCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**GTGA**TT  
 CTGCCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT  
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAAGTCAAGGC  
 CTACAGCTGTGTTGTTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTTGAATTTGAATTAA  
 CTTAGAAATTCATTTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA  
 AGTGGTCCGTGGTGTGTATTGGACAGCACAGAAAAAGATTTCCATCACCCACAGAAAGGTC  
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA  
 TGGAGTTTACTGTTTGTGAATAAAAAACGGCTGTTTCCGTGGAAAAA

**FIGURE 238**

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY  
RLFPPKALGQLISKYSLRELHLSFTQGFWRTTRYWGPPFLQAPSGAELWVWFQDVTVDVDSWK  
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK  
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTLVVFDAFITG  
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT  
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH  
PYRAFPVLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS  
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAKPVDWEESPLFNSLFPVSD  
GSNYFVRLYTEPLLNVNLTPTDFSMFYNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA  
KRLANLIRRARGVPPL

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**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCCTGTGAAGGAAGTGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCAGGC  
TCCTCCTCTACCAGGTGTCCTCAGAAATTGATGCTGGGTCCTTTCTACCTCTGGGGGTCACCTC  
TCACTTGGCACCTGCCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG  
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC  
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT  
TTGCTGTTTATAATCCAA

## **FIGURE 240**

MGSSSFVLVMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC  
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

**Signal sequence:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 27-33, 32-38, 102-108

**WAP-type 'four-disulfide core' domain signature:**

amino acids 49-63

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**FIGURE 241**

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG  
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC  
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCCTGCCTGTGGAGATGCAGGCCACTGAGCCAAAG  
 CGTCCAGTGGTCTTGTCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTA  
 TTAAGGAGCCTCAAACAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGCTCT  
 CTACAGTCCCTGGCAAAGCCTAAGTCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA  
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA  
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC  
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC  
 ACCCAGAGGGCAAGATGCAGGGATGGCTCTGTGCAGGACAGAGGCACAATCATGGAAGAGCC  
 AGGACACAAAGACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG  
 GTGTGAGAGAAGCACAGGGCAAAGCGGCAACCAGCCAAAGACGCTCATTCCAAAGATCA  
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA  
 CAGCAGTCATCCCACTTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAG  
 AGCCCCACGACGCAGAGAAACCAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG  
 GGATTTTGAAGAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG  
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAAACTCTTTCTGCCCAACCTCACTCTC  
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC  
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCTCCAG  
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGT  
 GCCGTGTTGGGCAACGGGGGCGATCCTGAACAACCTCCACATGGGGCCAGGAGATAGACAGTCA  
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC  
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT  
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCTGCTACTTGCACTTCTCTGGAAGGCAC  
 CCGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT  
 TCTGGTTGAGGCACAGACCCCGAAGACTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG  
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTCTGAGGCTCAAGACCTGGA  
 TGGTGCCCACTGGAGGATATACCGCCCCACCCTGCGGCCCTCCTGCTGCTCACTGCCCTTC  
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT  
 CACTACTATGATACATCATGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCTGGTC  
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCTGGTC  
 CCGGAAC TGCCAAAGCCAAGAAC**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCCCTGCTC  
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA  
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT  
 GGCAATGGCTAATTGAGGTTCTGAAGTTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG  
 GATTTTTAATTAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT  
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTCAGAAAAATATAGATCTG  
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC  
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGCTCTATACTTGTCCCTG  
 TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAACTGATAATAATACAAATGATTGTT  
 GTCCATGGAAGGCCAAATAAATTTTCTACAGTGAAAAA

**FIGURE 242**

MRSCWLRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLSQLAKP  
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW  
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGGGQTRKLTASRTVSEKHQG  
KAATTAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIPPEKKKPQATPPPAPFQSPTTQRN  
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF  
NQSEWDRLEHFAPPFGEFMEINYSLVQKVVTRFPPVPQQQLLLASLPAGSLRCITCAVVGNGG  
ILNNSHMQEIDSHDYVFRSLGALIKGYEQDVGTRTSFYGFTAFSLTQSLILGNRGFKNP  
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLPDFL  
RYMKNRFLRSKTLDDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYYDTSW  
KRLIFYINHDFKLEREVWKRHLHDEGIIRLYQRPGPGTAKAKN

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

**FIGURE 243**

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT  
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG  
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTTGTATGTTGTTG  
ACAGTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT  
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGCATGGAGGATAAGTGA GCAGACCGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG  
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTTGTATGTTGTTG  
ACAGTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

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**FIGURE 244**

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

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MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

**FIGURE 245**

GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG  
CCCCACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGCCGCGCCG  
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGACTGCCT  
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGTTTAACTGCGAGTTCTTCACCTTCT  
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG  
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT  
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT  
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC  
CCAGTGCGAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC  
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC  
CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC  
TGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT  
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA  
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA  
ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG  
GAGATGACAGCCTGGGTCACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG  
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT  
TCCGTGAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG  
CTAGATTAAAGCTGTAAAGACAAA

**FIGURE 246**

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTCCGTCYHRYC  
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSF  
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP  
YMPPQPSYPGA

**Transmembrane Domains:**

amino acids 10-28, 85-110

**N-glycosylation Site:**

amino acids 38-41

**N-myristoylation Sites:**

amino acids 5-10, 88-93



GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGCGCAAGGGTGAGGGCGGCCCCAGAA  
 TCCAGGCTAGGTAGCAGCAAGAAAGTGGTGGTGGTTCGCCCTCAAAATGGTGCCCTTGCACCATG  
 CTCTATTCTACTTTCTCAGTCTTGCTCTCTTAAGTGTGTCCACTCCTTCATGGTGTCAGAG  
 CACTGAAGACTCTCCAAAAGCTAGTAGTGAGGGACACCAATTCCTTGGAAATAAAATACGACTCT  
 CTGAGTAGCTCATCCAGGTTCATATGATGTCCTGTGATCATGCAAACTTACACAGCTGACC  
 TTCTGGGGAACGCAAGAGTAGAAATCACAGCCAGTACGCCACACAGCAACCATCATCTGCA  
 TAGTACACCCTGCAGATATCTAGGCCACCTCAGGAAGGGAGCTGGAGAGGGCTATCCG  
 AAGAACCCTGCAAGTCTGGAACACCCCCCTCAGGAGCAAAATGCATGCTGCTGCCGAC  
 CCCCCTCTTGTGGGGCTCCCGTACACAGTGTCTATTCATCTAGTGGCAATCTTGGAGA  
 TTTCACGGATTTTACAAAAGCACTACAGAACCAAGGAAGGGAACTGAGGATACTAGCA  
 CAAACAAATTTGAACCCACTGCAGTGAAGTGGCCTTCCTCGCTTGGATGAACCTGCCCT  
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCAAGGACCTAGCCATCTCCAATATGCC  
 ATTGTGGAATCTGTGACTGTGTGTCGAAGACTCATAGAAGACATTTGATGTGTCAGTGTGA  
 AGATGACCACTATCTGGTGGCTTCATCTATTCAGATTTGAGTCTGACGAAGAATAAAC  
 AAGAGTGGAGTCAAGGTTCTGTTTATGCTGTGCGCAGACAAGATTAATCAAGCAGATTATGC  
 ACTGGAGCTGCGGTGACTCTTGAAGATTTATGAGGATTTATGACATACCGTATCC  
 TACCCAAACAGAGATCTGCTGCTATTCCCGACTTTTCAGTCTGGTGCTATGGAAATCGGGGA  
 CTGACACATATAGAGAATCTGCTGTGTTGATGACAGAAAGCTCTTCGCACTCAAGTAA  
 GCTTGGCATCAGAGTGAAGTGGCCCATGAAGTGGCCACCAAGTGGTTTGGGAACCTGGTCA  
 CTATGGAATGGTGGATATGCTTTGCGTAAATGAAGGATTTGCCAAATTTATGGAGTTGTG  
 TCTGTGAGTGTGACCATCTGAACTGAAAGTGGAGATTATTTCTTTGGCAAAATGTTTGA  
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCTGTGTCTACACTGTGGGAAATCCGT  
 CTGAGTCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGAGCTTGATTTCTGAATG  
 CTAGAGGGAGTATCTTGCGCTGACGCATTTAAAGAGTGGTATGTACAGATTCTCCAGAAGCA  
 TAGCTATAAAATACAAAAGACGAGCTTGGGATAGTAGGCAAGTATTTGCCCTACGA  
 ATGGTGTAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATCATCTCTCTCTCAT  
 TGGCATCAGGAAGGGGTGGATGTGAAACCATATGCAACACTTGGACATGCAAGGGGTCT  
 TCCCTTAATAACCATCAGATGAGGGGGAGGAATGTACACATGAAGCAAGACATCATGA  
 AGGGCTCTGACGGCGCCCGGACACTGGGTACTCTGGGCATGTCTCAATGCATTCATCACC  
 AGCAATCCAACATGTGCTCATGATTTTGTCAAAAACAAAACAGATGTGCTCATCTCCC  
 AGAAGAGGTGGAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGTCATTAG  
 AGGATGATGGAATGGACTCTTTGACTGGCCTTTTAAAGAGAACACACACAGCAGTACGACAGT  
 AATGATCTGGGCAAGTCTCATTAACAATGATTTTACGCTCTGCAGATTTGGGAAGTCTGCAT  
 TGAAGAGCCCTTGGATTTATCCCTGATCTTTGAAACATGAAATGAATTTGCCGTGTTTTC  
 AAGGTTTGAATGAGCTGATTCCTATGTATAGTTTGAAGAAAGAGATGATGAATGAAGT  
 GAAACTCAATTCAAGCCCTCTCATCAGGCTGCTAAGGACCTCATGATAAGCAGACATG  
 GACAGCAGAGGGCTCAGTCTCAGACGAAGTCTGCGGAGTGAACACTACTCTCTGCCCTGTG  
 TGCACTAACTATGACCGTGCCTGACAGAGGGCAGAGGCTATTTCAAGATCTGGAAGGAATCC  
 AATGGAACCTTGAGCCTGCTGTGACAGTGAACCTTGGCAGTGTTCCTGTCAGTACTGAGAAA  
 CACAGAAGGCTGGGATTTCTTTATAGTAATAATCAGTTTCTTTCTGTCAGTACTGAGAAA  
 GCCAAATTTGAATTTGCCCTCTGCAAGAACCAAAATTAAGGAAAGGCTTCAATGGCTACTAGAT  
 GAAAGCTTTAAGGGAGATAAAATAAAATCAGGAGTTTTCAGCAAAATCTTACTACTATTGG  
 CAGGAACCCAGTAGGATACCCACTGGCCTGCAAAATTTCTGAGGAAAACTGGAACAAACCT  
 TACAAAAGTTTGAACCTTGGCTCATCTTCATAGCCCACTGGTATGGGTACACAAATCAA  
 TTCTCCACAAGAACCGGTTTGAAGAGGTAAGAGATCTTCAGCTCTTTGAAGAAAGATGG  
 TTCTCAGCTCCGTTGTGTCACACAGCAATTAAGAACCTTGAAGAAACATCGTTTGGATGG  
 ATAAGAATTTGATAAAATCAGAGTGTGGCTGCAAGTGAAGAGCTGAAGTATGCTTAAATA  
 TTCTCTCCCTGGCCGGTTCCTGTTATCTCTAATCAACAACATTTTGTGTAGTGTATTTTCAA  
 ACTAGAGTACTGGCTTTTGTGGCTCCAACTGGAGATACCTATTTTCCCTTCAACTATTTTTCGA  
 CTATCCCTGTGAAAAGAAATAGCTGTAGTTTTCATGAATGGGCTTTTCTGAATGAATGGGCTA  
 TCGCTACCATGTGTTTGTTCATCAGAGTGTGGCCTGCACGTAACCAAGTGTGGGT  
 TCCCTGCCACAGAAGATAAAGTACCTTATTTCTCTCAAAAAAATAAAAAAAAAAAAAA

**FIGURE 248**

MVFLPLKWSLATMSFLLSSLLALLTVSTPWCQSTEASPKRSDGTFPPWNKIRLPEYVIPVH  
 YDLLIHANLTTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE  
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA  
 ARMAFPCFDEPAFKASFSEIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA  
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA  
 IPDFQSGAMENWGLTTYRESALLFDAEKSASSKLGITVTVAHELAHQWFGNLTMEWWNDL  
 WLNEGFAKFMEFVSVSVTHPELVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD  
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGD  
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD  
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVMNGYYIVHYEDDGWDSL  
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEMPVFQGLNELIP  
 MYKLMKRDMMNEVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV  
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC  
 RTQNKEKLQWLLDESFKGDKIKTQEFPPQILTIGRNPVGYPLAWQFLRKNWNKLQKFELGS  
 SSIAHVMGTTNQFSTRTRLEEVKGFFSSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR  
 VWLQSEKLERM

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360



**FIGURE 249**

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC  
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCACAGCGGCTTGGGGTGCCAGGA  
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCCTCTCCCTGATC  
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACACCTCGTTAACTCCCTCCCGCT  
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGCTATGG  
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA  
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGGACCACCATTATGACACACGGAAAC  
 TTGGCTCAAGAACCACCTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
 GTGTGAGGAGACGTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG  
 GCTGCAGCACTGTTGGGGCTCAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
 GTGCTTGTTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTG  
 CTACCTGTGTGAGCCCCCTTGGAACTGTTCAAGTGCGCTCCCCCGAATGACCTGCCCCAGG  
 GCGGCCACTCATTTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT  
 GAGCATTAGGGCTGCGTGGCCCAACCTTCAGCTTCTTGTGAACCACACCAGACAAATCG  
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
 GTGGGGAGTGTTTTGCCCTTCCTGCT**TA**ACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTT  
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTACCTAACAGCA  
 AACTGGGGAGAGCCTGGAGCATCCGGAAGTTCCTATGGGAGAGGGGACGCTGGAGGAGTG  
 GCTGCATGTATCTGATAATACAGACCTGTCTTTCA

**FIGURE 250**

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGRGGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSTNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC  
PSC

**FIGURE 251**

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT  
CAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCCTTCCTGTCACTGCTG  
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG  
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG  
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCA  
GGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC  
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
CGCCACGCTGTCCTGCCAGGGCCGCGGGGACAGCTGAGCATGCCCAAGGACGAGGCTGCCA  
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTATCGGCATCAAC  
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA  
GTGGCGCAGCGGTGAGCCCAACAATGCCACGACGAGGAGGACTGCGTGGAGATGGTGGCCT  
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAA  
GAGAACATGTGAGCCTCAGGCTGGGGCTGCCCATTTGGGGGCCCCACATGTCCCTGCAGGGTT  
GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG  
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG  
AAAGTGTTCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC  
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 252**

MRGNLALVGVLLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG  
PTGEKGDMDGDKQGKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPLPCECSQLRKAIGE  
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN  
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTTFNKWRSGEPPNNAYDEEDCVEMVAS  
GGWNDVACHTTMYFMCEFDKENM

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MRGNLALVGVLLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG  
PTGEKGDMDGDKQGKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPLPCECSQLRKAIGE  
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN  
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTTFNKWRSGEPPNNAYDEEDCVEMVAS  
GGWNDVACHTTMYFMCEFDKENM

**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGTCTAGCCAGTTCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCTTGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCAGAAACGTGACATGCATGACTTCTTGTGGGACTTATGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGCCCC  
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT  
ATCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC  
TTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT  
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTTGGTGTGGAAATGCA  
TAGTGAATATCCCCAACCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTGTAGTGT  
CCTACATTAATAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 254**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLQQLQRLFKSHSSLEGLLK  
ALSOASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGFPLPSVRVPRPLHPNQLGSTGK  
SSLGTEEQRPRL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

**FIGURE 255**

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGTGTGCCCGCTGTGCCTGCTGTGCC  
 CGCGCTGTCCGCGCTGTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG  
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC  
 CCATAGTTGCTGCAGGAGTGAGGCCATGAGCTGCGTCTGGGTGGTGTATCCCCTTGGGGC  
 TGCTGTTCTCTGGTCTGCGGATCCCAAGGTACCTCCTGCCCAACGTCACTCTCTTAGAGGAG  
 CTGCTCAGCAAATACCAGCACACAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA  
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT  
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGACAGGCTGGCACCAGGGGGTGGGGC  
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG  
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTGTTGTT  
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCATGCCCTG  
 AAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG  
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT  
 TGCCAGGCTGGTCTTGAACCTCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG  
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA  
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACCTCTGGTAGC  
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG  
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC  
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCTCGCGTGGTTGCCATGACT  
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCTTAGG  
 CTTTGCTAACCGGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT  
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG  
 TGGAAACTTCTTCTTGCTGGTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG  
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGCCATCCGTCAGTATGAATGGCTT  
 TTTAAACAAACCCACGTCCCAGCCTGGGTAACATGGTAAAGCCCCGTCTCTACAAAAAATC  
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG  
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC  
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

## **FIGURE 256**

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTILLELLSKYQHNEHSRVRRAIPREDKEEILML  
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR  
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 27-31, 41-45

**N-myristoylation site.**

amino acids 126-132, 140-146

**Amidation site.**

amino acids 85-89



**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGG  
GTCTGGGCTGCCCCCTTGTCTCCTCTTGACCCCTCTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTG  
TGTCTTCTTGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCTGTCTTT  
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG



**FIGURE 259**

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT  
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT  
**TATG**ATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC  
TATTAATATTTACCATTGCAGAAGCTTCATTTCAGTGTTGAAAATGAATGCTTAGTGGATCTG  
TGCCCTCTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCCCTCCC  
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACCTTTTTTT  
TTTTCTTGGCATAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA  
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTGGGCTATCAATATTACTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC  
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA  
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA  
ATAAAAGTTCATATCTACCC

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**FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP  
SDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

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**FIGURE 261**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT  
 GAGAAGAGCCACAGCATTAAGAGACTGCCCTGCTTGGTGTTCCTGAGGATGATGGTGGCCCTT  
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCTTGCAGCTTTCTGCCCCCGCAGTGTAC  
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGGACAAGGGCTGG  
 AAAAATGTACCCAAGCAACGAGGGCATACATTCAAGAATTCGAAGAGTTCACAAAAATATA  
 TCTGTCATGCTGGGAAGATGTACAGACTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTT  
 GGCACTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG  
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA  
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACTGCTGATGGGCATAAAGTC  
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA  
 ACTCTCCAAGGTGTAATTTAATTTGGATCCAGAAACAACACTGTTGGGAATTTGCAAAAC  
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCGGAAGCAAATCCTAACCTTTT  
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT  
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA  
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCTCCTCAACTTACATTGACCTGGCTGT  
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGGTTCTCA  
 CAAAGATTGAGCCGGGCACATGGGAGTGGAGCATTTCATGGGATACCCCATGCAGAAGCCAG  
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGCCCA  
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCATCATAGTGGAGGAGCTTGG  
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT  
 AAGCAGCTCTATGCCCTGGAATGAAGGAAACCAGATCATTTACAACCTCCAGACAAAGAGAA  
 GCTGCCTCTGAAGTAAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT  
 TACAGGACAGTGAGGCTATAGCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG  
 AGTGTGTAGAAGTGGAAATACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTC  
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAA  
 CCTCCTGGCTCTCAAGGATGACCACATTCCTGATACAGCCTACTTCAAGCCTTTTGTCTTACT  
 GCTCCCCAGCATTCTACTGTAACCTGCCCCTCTCCCTCCCAATTAGAGTTGTATGCCAGC  
 CCCTAATATTCCACCTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTT  
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCACTAAAATACTATTAAATATTTCTTT  
 CTTTCTTTTTCTTTTTTTTTTGGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC  
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC  
 CACACCTGGCTTAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTG  
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAATAATTAACATTTGAATATCGCTTT  
 CCAGGTGTGGAGTGTTCACATCATTTGAATCTCGTTTACCTTTGTGAAACATGCACAAG  
 TCTTTACAGCTGTCTTCTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC  
 TAGAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT  
 TGTTCCACTACTCTTATAGTCAATGCGTTTATCGTTTTCAGCCTAAAAATAATAGTCTGTCCC  
 TTTAGCCAGTTTTTCATGCTGCACAAGACCTTTCAATAGGCCCTTCAAATGATAATTCCTCC  
 AGAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTGTCTGCTCTCTGTT  
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

MMVALRGASALLVFLAFLPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE  
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLRADCEIVSEDKTLAEMLL  
QEAEEEKKIRTLNLNASCNDNLMGIKSLKIVKKMMDTHGSMWKDAVYNSPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPA PRKQILTLWSWQGTGQVIYKGLFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT  
PCRSQDAEASFLLCGVLVYVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH  
YNPRDKQLYAWNEGNQIIYKLTQRKRLPLK

**FIGURE 263**

GGGCGCCCGCTACTACTAGCTGAGGTGGCAGTGGTTCACCAACATGGAGCTCTCGCAGA  
 TGTTCGAGCTCATGGGGCTGTGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG  
 GTAGCGCGGGGTGGCTGCGCGCGGGGAGGAGAGGAGCGCGCGCGCTGCCAAAAAGC  
 AAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTC  
 GGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC  
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC  
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCTGCAGCGAGAGCACCGCAGCA  
 TGAGAGCCAACCTGGAGCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCC  
 TTCATCGTCTGGCTGGCCAACGGGGACACCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA  
 TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAAGCGCCTGTCA  
 TCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCCTCCAGTGACACCACTGTC  
 CTCATCTGGAGCCTGAAGGCTCAAGTGTGTCTACCATCAACACCAACCAGATGAACAACAC  
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGA  
 AGGTTTGGGAAGTCTGCTTTGGAAGAAGGGGGAGTTCCAGGAGTGGTGCGAGCCTTCGAA  
 CTAAAGGGCCACTCCGCGCTGTGCACTCGTTTGTCTTCCAACGACTCACGGAGGATGGC  
 TTCTGTCTCCAAGGATGTTACATGGAACCTGTGGGACACAGATGTGGAATACAAGAAGAAGC  
 AGGACCCCTACTTGTCTGAAGACAGGCCGCTTTGAAGAGCGCGGGTGCCGCGCCGTGCCG  
 CTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCTCTCTA  
 CAATACCCGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGTCATGGCGAGTGTATCGCCA  
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGACCGGGCGGTGCGGCTG  
 TTTCACAACACTCTTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC  
 CTCCAACGAGAGCACCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCCAAGAGACCTGA  
 AGAGCCTGGGTGCCCTGAAGAAGTGACTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGAG  
 GGATCTGGCTCCTCATGGCACTGCTGCCATCTTTCCTCCAGGTGGAAGCCTTTCAGAAGG  
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTT  
 AGGTCTCTCTCTTCTTGTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGTGCTTTTCTTCT  
 CTCCAGGCCAGTGGGTGGAATCTGTCCCACTGGCACTGAGGAGAATGGTAGAGAGGAG  
 AGGAGAGAGAGAGAGAATGTATTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAAG  
 TTTGTAAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTGTCAAGGA  
 TGGGAGACTGGGATAGCTTCCCATCACAGAACTGTGTTCCATCAAAAAGACACTAAGGGATT  
 TCCTTCTGGGCCTCAGTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCA  
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT  
 AGTACTATTGTCCAATGTGATGAAGTGGTAAAAGTGGGAACCACTGTGCTTGAACCAAA  
 TTAGAAAACACATTCTTGGGAAGGCAAAAGTTTCTGGGACTGATCATACATTTTATATGGT  
 TGGGACTTCTCTCTCGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAAGTTTATCAAG  
 TTCATCAGATATTTGAGTGCCCACTCTGTGCCCAATAAATATGAGCTGGGGATTAATAA  
 AA

**FIGURE 264**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK  
QYQIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWS TKDFLQ  
REHRSMRANVELDHATLVRFS PDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK  
HKAPVIDIGIANTGKFIMTASSD TTVLIWSLKGQVLSTINTNQMNNTHA AVSPCGRFVASC G  
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSA AVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNT PGHRAMVEEMQGH LKRASNESTRQRLQQQLTQ  
AQETLKSLGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308



**FIGURE 265**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC  
TCCTAGTAACCTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT  
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT  
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA  
AGCACACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGACGGCAGGTAC  
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCTGGTCTCAGGATACCCA  
CCATCCTTTTCCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC  
TCTCCCAGTCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAG  
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCTGAGGATGTACAGCTTGAGG  
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTA  
AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTCTTCTGGGCCCTG  
CCCCCTCTCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT  
GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTACGTGAGGTCTGTGAGG  
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC  
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTACCCCAAGGCAGGTGTAGGGAGCCCCA  
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA  
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT  
TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA  
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCCTTAAACAACTCCTTTCCA  
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG  
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG  
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

**FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHP  
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNNF

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

**FIGURE 267**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTTCTTTC  
CTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC  
TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG  
CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA  
GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT  
CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG  
TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT  
TTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT  
GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG  
GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTGGGGGAGTTTTCGTGGTGGGATCA  
GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT  
TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGAT  
TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATT  
GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA  
TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA  
CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA  
TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG  
TGAGCAAGTCACTTGAGGTCGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC  
TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG  
GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA  
CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

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**FIGURE 268**

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSM LDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGE GFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 269**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG  
GGCCAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG  
CTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG  
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG  
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC  
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCTCTCTGGGCAGTCAGATCCACCCAG  
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG  
GCTATTCACTTTTATATATTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV  
VFSLLAALLLAVGLALLVRKLRKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV  
VFSLLAALLLAVGLALLVRKLRKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**FIGURE 271**

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTGGGGT  
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACTATTATTATTGTTG  
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAACCCACAGGCAAGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTAAATTCCTGGTGCTGAAGCCTGGGGCAGGGGTGTAAGAAAAACACTTAGATCAATG  
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT  
TTATTAATTTTTAAAATCAGTAAGTATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAA  
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA  
AGAAGGGAAAATGTTGCCAAGGAAAAAAA

**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSENTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

MTFFLSLLLLLVCEAIWRSNSGSENTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT



**FIGURE 273**

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTTATTTCAGAGGTTTGTGTTTCCTCTTAGTCT  
 GTGCCTGCTGCACCACTCAAATACTTCCTTCATTAAAGCTGAATTAATAATGGCTTTGAAGATA  
 TTGTCAATTTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT  
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA  
 TGATCTATATAATTAACTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAAACATG  
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCA  
 TACACCAAGCAGTTTCACAGAATGTGGAGAGAAAGCGAATACATTCACTTCACCCCTGACCT  
 TCTACTTGGAAAAAACAATAATGATATGGACCACCAGGCCAACTGTTTGTCCATGAGTGGG  
 CTCACCTCCGGTGGGGGAGTGTTTGATGAGTACAAATGAAGATCAGCCCTTCTACCGTGCTAAG  
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAA  
 GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAAACAAACTGTATG  
 GAAAAGATTGTCAATTTCTTTCCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTTATG  
 CAAAGATTGATTCTGTGTTGAATTTGTAACGAAAAAACCCATAATCAAGAAGCTCCAAG  
 CCTACAAAAACATAAAGTCAATTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT  
 TTA AAAACACCATACCCATGGTGACACCACCTCCTCCACTGTCTTCTATTGCTGAAGATC  
 AGTCAAAAGAAATTTGTGTGCTTTAGTTCTTGATAAGTCTGGAAGCATGGGGCTAAGGACCGCT  
 AAATCGAATGAATCAAGCAGCAAAAACATTTCCCTGCTGCAGACTGTTGAAAAATGGATCCTGGG  
 TGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAATAAGCTAATCCAAATAAAAAGC  
 AGTGATGAAAGAAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACCTCCAT  
 CTGCTCTGGAATTAATATGCAATTTCAAGTGATGGAGAGCTACATCCCAACTCGATGGAT  
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTTGTATTGATGAAGTG  
 AAACAAAGTGGGGCCATTGTTGATTTTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT  
 AGAGATGAGCAAGATAACAGGAGCAAGTCATTTTTATGTTTTCAGATGAGCTCAGAACATG  
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAGTCCCTT  
 CAGCTCGAAAGTAAAGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCAATAAT  
 TGATAGTACAGTGGGAAAGGACACGTTCTTTCTCATCAGATGGAAACAGTCTGCCCTCCAGTA  
 TTTCTCTCTGGGATCCCAAGTGGAAACAAATATGAAAAATTCACAGTGGATGCAACTTCCAAA  
 ATGGCCTATCTCAGTATTCAGGAACCTGCAAAGGTGGGCACTTGGGCATACAATCTTCAAGC  
 CAAAGCGAACCCAGAAACATTAACATATTACAGTAACCTTCTCGAGCAGCAAAATCTTCTGTGC  
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAACAGTTTCCCGAGCCCAATGATT  
 GTTTACGCAGAAATTTACAAGGATATGTACCTGTTCTTGAGGCAATGTGACTGCTTTTCAT  
 TGAATCACAGAAATGGACATACAGAAGTTTGGAACTTTTGGATTAATGGTGCAAGCGCTGATT  
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAATGGCAGATAT  
 AGCTTAAAGATTCGGGCTCATGGAGGAGCAAAACACTGCCAGGCTAAATTTACGGCTCCAT  
 GAATAGAGCCGCGTACATACCAGGCTGGGTAGTGAACGGGGAATTTGAAGCAAAACCCGCCAA  
 GACCTGAAATTTGATGAGGATACCTCAGACCACCTTGGAGGATTTAGCCGGAACAGCATCCGGA  
 GGTGCATTTGTGGTATCACAACTCCCAAGCCTTCCCTTGCCAGCAATCCCAAGTCA  
 AATCACAGACCTTGATGCCACAGTTTCATGAGGATAAGATTATTCTTACATGGACAGCACAG  
 GAGATAATTTTGTGTTGGAAAAAGTTCAACGTTATATCATAAAGAAATAGTGCAAGTATTCTT  
 GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTATGATCTGTCCACAAAGGA  
 GGCCAACTCCAAGGAAAGCTTTGCAATTTAAACAGAAAAATATCTCAGAGAAATGCAACCC  
 ACATATTTATTGCCAATGAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT  
 GCACAAGTAACCTTGTTTATCCCTCAAGCAAATCCTGATGACATTGATCCTACACCTACTCC  
 TACTCCTACTCCTACTCTGATAAAAAGTCATAAATCTGGAGTTAATATTCTACCGTGGTAT  
 TGTCTGTGATTTGGGCTGTGTTGAATTTGTTAACTTTATTTTAAAGTACCACATTT**TGA**ACCTTA  
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAACCAATGTAAGT  
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAACTCATAAAAATTAAT  
 TTAAGATTGTCGGAAGAGGATCTTTGATTAATAAAAAACACTCATGGATATGAAAAACTGT  
 CAAGATTAAATTTAATAGTTTCAATTTATTTGTTATTTTATTTGTAAGAAATAGTGTGAAC  
 AAAGATCCTTTTTCATACTGATACCTGGTTGTATATTGATAGTCAACAGCTTTTCTGAAT  
 GATATTTCAATTTGCATCAAGAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAAA  
 GGAGAGCAAAATAACAACATTTGGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 274**

MGLFRGFVLLVLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKII EQIEDMVT TASTY  
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC  
 GEKG EYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPPYRAKSKKIEATR  
 CSAGISGRNRVYKCGGSGCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE  
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSED FKNTIPMVT P P P P P V F S L L K I S Q R I V C L V  
 LDKSGSMGGKDRNLNRMQAAKHFL LQT VENG S W V G M V H F D S T A T I V N K L I Q I K S S D E R N T L M  
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLL L T D G E D N T A S S C I D E V K Q S G A I V H  
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT  
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG  
 TAKVGTWAYNLQAKANPETLTITVTSRAANS SVPPITVNAKMNDVNSFPSPMIVYAEILQG  
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVBRAHG  
 GANTARLKLRLPLNRAAIYPGWVNGEIEANPPRPEIDEDTQT TLEDFSR TASGGAFVVSQV  
 PSLPLPDQYPPSQITDL DATVHEDKIILTWAPGDNFDVGKVQRYIIRISASILDRLDSFDD  
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAKSIDKSNLT SKVSNIAQVTLFIP  
 QANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 275**

CTCCTTAGGTGGAACACCTGGGAGTAGAGTACTGACAGCAAGACCGGGAAAGACCATACGTCCTCCCG  
GGCAGGGGGTGAACACAGGTGTGCATCTTTTGTATCTCGTGTGGGTCGCTTCTATTTCAAGGAAAG  
ACGCCAAGGTAAATTTGACCCAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACC  
CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT  
TGTGTTGGAGGAGAGAACCCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGCTTGCCTGA  
GGGTGGACAGAAAGAAAGGAAAGTCCCTCTTGTCTGTTGGCTGCACATCAGGAAGGCTGTGATGGG  
AATGAAGGTGAAAACTTGGAGATTTCACCTTCAGTCATTGCTTCTGCCCTGCAAGATCATCCTTTAAAA  
GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCGAGAAGCTCGTTCTAGAAGGAAATGGATG  
CAAGCAGCTCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAAGCCCTTCCGTGGG  
GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCCCTGAATGATGTTTCCG  
GGGGGTGCTTGGGTGATTTCGCCGGTGGTGGTTTGTGCTGGTGCTCTCTGCTGTGCTATCTCTGT  
CCTGTACATGTTGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCACTGCCACGGGGCAACAGC  
CCCACGGGGAGGAGGGGTACCAAGCCGCTCCTTCAGGAGTGGGAGGAGCAGCACCCGAACTACGTGA  
GCAGCTGAAGCGGCAGATCGCACGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAA  
TGGGCAATACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAAACCCAG  
GCCAGCTCCTGGCCTTCTGCACTCGCAGGTGGACAAGGCGAGAGTGAACTGCTGGCCTCAAGCTGG  
CCACAGAGTATGACAGCTGCTTTTCGATAGCTTACTCTACAGAAAGGTGTACCAGCTGGAGATGG  
CCTTACCCGCCACCCGAGGAGAAGCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGGAAGCCATT  
GAATCAGCTTTGGAGACCTGAACACTCTGCAGAGAAGCAGCCCAATCACCCTCCCTTACCGCCCT  
CTGATTTTCATGAAGGGATCTACCGAACAGAAAGGGACAAAGGACATTTGATAGAGCTCACCTTCAA  
AGGGGACCAAGAACAGAAATTAACAGGGCTCATCTTATTTCGACCATTCAGCCCCATCATGAAAGT  
AGGAGTCAAAAGCTCAACATGGCCAAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGG  
ACAAGTCTCCGGCAGTTCTATGCAGAAATTCAGGGAGATGTGCATGTAGCAGGATGGGAGATGCTT  
CACTGTTTGTACTTTTGGGAAAGAAGAAATAAATGAATCAAGGAATACCTTGAAGAACCTTCCAAA  
TGCTGCCAAGTTCAGGAACCTTACCTTATCCAGCTCAATGGAGAAATTTCTCGGGGAAGGGACTTG  
ATGTTGGAGGCGCGCTCTGGAAGGGAAGCAACGCTCTCTTCTTGTGTGATGTGGACCTTACTT  
CACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAGGATTTTATCCAGTT  
TTTTTCAGTCAGTACATCCCGCATTAATATCGGCCACCATGATGCAGCTCCCTCCCTTGGACAGC  
AGCTGCTCATAAAGAGGAAACCTGGATTTTGGAGAGACTTTGGATTTGGGATGAGCTGTGATTCG  
GTCAGACTTCATCAATATAGGTGGGTGTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC  
CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGACCGCTGTGCGAGGACTTCCACC  
TCTGGCATGAGAAGCTGCATGGAGCAGCTGACCCCCGAGCGTACAGATGATGATGATGATGATGATG  
GGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTGGTGTCTAGGCACGAGATGAGGCTCAC  
CTTCGCAAAACAGAAACAGAAAGCAAGTAGCAAAAAAATCAAGCTCCACAGAGAAGCAATTTGGGAGA  
CACTTTTTTCTTCTTTTGTCAATTTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAAGGACG  
ACAAAAGAATTGGACTGATGGGTGCAGAGATGAGAAGCCCTCCGATTTCTCTCTGTGGGCTTTTAC  
AACAGAAATCAAAATCTCCGCTTGGCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACA  
AAGGCAGAAATGCTTGTGAGATTATAAGCCCTAATGGTGTGGAGGTTTGTAGTGGTGTTCACATACACT  
GAGACCTGTTGTTTTGTGTGCTCATTTGAAATATTCATGATTTAAGAGCAGTTTGTAAAAAATTCAT  
TAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGAGCCTTAGCAGGCGCTTGTGTTCTAGG  
AATGCTAAAAATATCAAGAGCAGGAGAGGAGATAGGCTTATTATGATAGTGAAGTACATTAAGTA  
AAAAATAATGGACAGAAAAGAAAAGAAACCATAAATATCGTGTCTATTTTTCCCCAAGATTTAACCA  
AAAAATAATCTGCTTATCTTTTGGTGTCTCTTTTAACTGTCTCCGTTTTTTTTCTTTTATTTAAAAAT  
GCACTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGA  
GCACAAGTTGGCCTACATTTTTATATTTTTTAAAGAGATACCTTTGATGCTATTTAGAACCTTTCA  
GTTCAAGAGCATCAAAATGATGCCATTCGAAGGACATGCCAAATGCTGATTCGTGCAGGCATGAAT  
GTCAAGGATTTGAGATAGGGAAGGAATGGTGTGTACTAATACAGACGTACAGATACCTTTCTCTGAA  
GAGTATTTTCAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAA  
AAGGAAACTCATTAGACTGTTGATATCGTGATGTACCTTAAAGTCAGAAACCAACATTTTCTCTCTCA  
GAAGTAGGGGCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACCAACTCTCT  
TTTTCAAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATGAAGAGAAATGGAGAAAAATATATATAT  
ATATATATATATTTGAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAGTTTGTGCTATACAT  
GTTATCCACCCGAGGCGAGGTGGAAGTAACTGAATTTATTTTAAATTAAGCAGTTCTACTCAATCA  
CCAAAGTGTCTTTGAAAAATGCATTTTATACCAATTTCAAACCTATTTTAAAAATAAATACAGTTA  
ACATAGAGTGGTCTTCTTATTCATGTGAAAAATATTAGCCAGCAGATGATGATGAGCTAATTTATCT  
CTTTGAGTCTTGTCTGTTGTGCTCAGTAAACTCATTTGTTTAAAGCTTCAAGAACATTTCAAGC  
TGTGGTGTGTTAAAAAATGCATTTGATTTGTTGACTGTTGATTTATGAAATTTAATTTAAACAC  
AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

**FIGURE 276**

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVVKDKRDELVEAIES  
ALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP  
MKVKNEKLNMAANTLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR  
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI  
NIGGFDDIKGWGGEDVHLYRKYLSNLI VVRTPV RGLFHLWHEKRCMDELTPEQYKMCMQS  
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

**FIGURE 277**

GAAAGA**ATG**TTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTTCATGCTGAACTCTGTCAACC  
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT  
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTTCCATGAGAAAA  
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT  
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC  
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAT  
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG  
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT  
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT  
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG  
 GGGCATATTAATGATGCCTTCA**TGA**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT  
 TGTTCGCTTCCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA  
 CCAAGAGCAGATCATATATTTTGTTCACCATTCCTCTTTTGTAAATAAATTTTGAATGTGCT  
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCCTGAAATCATAAGCTATTCACGAC  
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAAATGTGGTCAATGTGGTATTTG  
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC  
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT  
 TGAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG  
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGAATT  
 TTATCCTGTTATCACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC  
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG  
 TAATAATCATCTCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 278**

MLWLLFFLVTAIHAE LCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP  
NREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLP AVEVQSAIRMNKNRINNAFFLNDQTLE  
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL LILSGIWQRRRKNKEPSEVDDAEDKC  
ENMITIENGIPSDPLDMKGGILMMPS

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MLWLLFFLVTAIHAE LCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP  
NREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLP AVEVQSAIRMNKNRINNAFFLNDQTLE  
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL LILSGIWQRRRKNKEPSEVDDAEDKC  
ENMITIENGIPSDPLDMKGGILMMPS

**FIGURE 279**

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG  
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCT**CATGT**  
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG  
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC  
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCCGTGGGTGATGCTCTAACAGTGACCTGGA  
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC  
 CAACCCATGAGTGGGCGGTTTAAGGACGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA  
 TGCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA  
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA  
 CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT  
 GTTTATTTAGAAGACACAGACT**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA  
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
 TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTTAAGGTCTTATTTAATTTCAGA  
 GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCTTAA  
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC  
 AATTTGTCTGTTACATTTCTTTTACGTATTCTTTTAGCAGCACTTCTGCTACTAAAGTTA  
 ATGTGTTTACTCTCTTCTTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG  
 TTTCTGATTAAACAGTAAATCCTAAATTCAACTGTTAAATGACATTTTATTTTTATGTCTC  
 TCCTTAACATATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT  
 TTTGTGC

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**FIGURE 280**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT  
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ  
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIQSACALMIIIVVVVLFQHYRKKRWAER  
AHKVVEIKSKEERLNQEKKVSVYLETD

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**FIGURE 281**

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT  
ACTCTTGAGGAGTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT  
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTT  
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTTCATGCTTCTTGATTC  
ATCCAACACTACTACCTTGCTACGATATCCCCTTTATCTCTAATCAGTTTATTTCTTTCAA  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

**FIGURE 282**

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATG PADDEAPDAETTA AATTATTAAPTAT  
TAASTTARKDIPVLPKWVGDL PNGRVCP

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MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATG PADDEAPDAETTA AATTATTAAPTAT  
TAASTTARKDIPVLPKWVGDL PNGRVCP

**FIGURE 283**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTTGCTGTTAAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGCCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG  
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTTAAAACCACAGGCTGG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAAACTGAGAAAT  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCTTGTCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

**FIGURE 284**

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG  
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWFPVGVARGGALCQ

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**FIGURE 285**

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA  
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG  
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC  
CGGGCCGGGATGCAGCCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA  
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC  
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCC**TGA**ATCTGCCTGGATGGAAGTGA  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCCCTGTGCAGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCACTTCTGAGCACAGAGCAGAGACAGAC  
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTTCATGCCTACACACCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK  
ARNSLGLYGRRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ  
IQR LH TAALPA

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**FIGURE 287**

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTGCAT  
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAGCCAGGA  
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC  
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC  
 TAAAGTTTACAAGAAATGTACCTTGCTTCAAGAGTTTGAAGCATTTCATGAGGCCAATG  
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACTCCGACGAAATCAACGCC  
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA  
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCACTGGG  
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACGTGTGTCTGTCTCCCAATCAGCTCAG  
 GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC  
 TAAATAGTCTTTTCTCAATGTGTCTCCAAGCAAGATTATCATAACTTATAGGTTTCATGA  
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTTATTAATAAAATTGCAACACAAGATCAAT  
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT  
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT  
 AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAAA  
 AAATCACAGTAGCAATGCAACTCATCTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT  
 TTCCCTTGGAAGTTTAGCGTATGTTTGAATAACAAAATTCCTTACATCAGAGACTCTAGGT  
 GCTATATAATCCAAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC  
 TTGTCAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT  
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTGATTTTTTTTTTTTCTTCATGCC  
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT  
 CAATTTTCATTTCCACCATTGCATTACAACCTCTAACTTAAATGGGTAACCTAAGGCATAT  
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT  
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCCCTTTTTTACATTT  
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT  
 TGGAAGCTGAAAAGTGAATTTAAAGAATGCTATCTTGGAATAATGCATACGTCTGTGCAATT  
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT  
 TAATATCAAATTACAAAGTTTAGACTTGAGGGGAAATGGGCTTTTGAAGCAAACAATTTT  
 AAATATATTTTGTCTTCAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT  
 CCCACTTGCAAACTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTCATTGCTCA  
 ATAATAAAGCCTGAATCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 288**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLDKTQIEKLWT  
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVI PRNSDEINALQ  
DYGKRS LPGVNDFWLGINDMVTGK FVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK  
WSDEACRSSKRYICEFTIPK



**FIGURE 289**

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCTCCGCGCGC  
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTGCA  
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG  
GAGTCGGCGGGCGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCT  
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT  
GTGTGGCTGAGCTGGGTCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG  
GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC  
CACCCGCGAGGGCTGAAAACCCCGCCGGGGAGGACCGTCCATCCCCTTCCCCGGCCCCCT  
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 290**

MKLAALLGLCVALSCSSAAAFVLGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLS  
SLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG

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**FIGURE 291**

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGACAGCTGAAGGGAGGCACT  
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCTCTG  
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCC  
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG  
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT  
 GCCAAGGAGACTTCAAACCTTCGGATTACGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG  
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA  
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG  
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAC  
 GGGCCTCTCACAGGGGAGTTTTCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT  
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA  
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAACT  
 GTTTGATGAGATTAATCCTGAAACCAAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA  
 AATGGTTGACCCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTAC  
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTGCTCCACCTTTGACAAGAA  
 TTTTCGTTGTCTATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA  
 TGGAGAAAATGGGTGACCACCTCGCCCTGAAGACTACCTGACCACAGACTTGGTGGAGACA  
 TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTTTCTTTCGGAAGTTCAGCTAGATCA  
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTG  
 CTGACCTTAGTGAACCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA  
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTAC  
 TGCTTATTCATGCTCCTGTCTCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG  
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTA**TAAT**TCAGG  
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA  
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTGTTCTTAACTAGTTTAGGGTGTCTC  
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC  
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT  
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA  
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA  
 CTAAGTGACTCATGGGCAGGAGCATAGACAGTGTGGAGACATTTGGCAAGGGGAGAATTCA  
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCACTACTCAGAATGGCATGC  
 TGCTTAAGACTTTTAGATTGTTTATTCTGGAATTTTTCATTTAATGTTTTTGGACCATGGT  
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAACCATGGATAAGGGAGGACTACTACAAA  
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 292**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E  
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I  
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F  
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P  
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L  
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A  
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F  
L G R V V N P T L L

**FIGURE 293**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG  
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG  
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG  
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGCTGTCCC  
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA  
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCC  
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC  
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA  
TCTACCACCCCACTAGTAGGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCAGG  
CTGTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA  
AAAAAAAAAAAAAAAA

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**FIGURE 294**

MRLLLLVTSLVVLLWEAGAVPAPKVPIKMQVKhWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLTTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE  
RRLWVMPNHQVLLGPPEEDQDHIYHPQ

**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGAGTGAGGGAGGGAGTGAAGGAGCTCTCTG  
TACCCAAGGAAAGTGACAGTGAGACTCAGACAAGATTACA**AATGA**ACCAACTCAGCTTCCTGC  
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
TAGTGACATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT  
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG  
CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG  
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG  
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
ATGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
GACGCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGGGGATT  
TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTTGTGCTGGAATGAGGG  
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCAGAGGCCAGT  
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATCATGTTGGTTA  
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTGTG  
GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTACCCA  
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

**FIGURE 296**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG  
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI  
YQKYPVKYGEKGCWTDNGFVIPVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAN  
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL  
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**FIGURE 297**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGTGCTTGGGCCG  
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC  
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC  
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC  
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACACGGTCACCACCATGAAACCTACAGCG  
GCATCTAATACAACAACACCGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC  
TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT  
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC  
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAATGTATTACTCAAGAAGAGGCATTCC  
GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA  
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTAAAAACAATATTCT  
CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA  
AAGATTCTTCAAGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT  
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAACAAGTCCTATCTTTTTTTTTTGGCT  
GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA  
TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT  
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG  
TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

**FIGURE 298**

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH  
TNETSNSTVKPPTSVASDSSNTTVTMMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN  
TSQISTSTMTVTHNSSVTSAAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTGLVLSILYIG  
CKMYYSRRGIRYRTIDEHDAII

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**FIGURE 299**

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCAGCCGGGAGCCGG  
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**CGCACCCCTGTGGGGAGGC  
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCTGCTGCTGCTGGC  
 GCAGCTGTGACACGCCCAAGAATTTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT  
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT  
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA  
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA  
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATCTGAAGAGG  
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT  
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG  
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
 CATGTTGTCTCTCAGCT**TAA**TTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA  
 CTGGAAGAAGTACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTACCAACT  
 GTTGCTGGAAGATTCAAACTGGAAGCAAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA  
 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTGG  
 TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA  
 AGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG  
 TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT  
 AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT  
 TCGAGTTTCATTTATATTTTGCACTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG  
 ACTTTTGCCTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT  
 CTAAATGCCTGGTGGCTTTTTCACAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG  
 CAATGCATCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
 GTGTGTGTGCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGACACT  
 TGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTG  
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC  
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATATTGGATAACTGGCTTTTT  
 TCTTCTATGTCCTCTTGGAAATGTAACAATAAAAAATAATTTTGAACATCAA

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**FIGURE 300**

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS<sup>1</sup>GH<sup>2</sup>IYNKNIS<sup>3</sup>  
QKDCDCLHVVEPMPVVRGPDVEAYCLRCECKYEERS<sup>4</sup>SVTIKVTII<sup>5</sup>IYLSILG<sup>6</sup>LLLLY<sup>7</sup>MVY<sup>8</sup>LT<sup>9</sup>L<sup>10</sup>  
VEPILKRRLFGHAQLIQSDDDIGDHQP<sup>11</sup>FANAH<sup>12</sup>DVLARS<sup>13</sup>SRANVLNKVEYA<sup>14</sup>QQRWKLQV<sup>15</sup>QEQ<sup>16</sup>  
RKSVFDRHV<sup>17</sup>VLS<sup>18</sup>

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**FIGURE 301**

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT  
CTGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCAAGGCCTTCCTGTCCCGGGGAAGCGG  
CAGGAGCCGCCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA  
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG  
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG  
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT  
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA  
TCATTGTCTACATTAAACTTCCTTAGTTTCATAAAATTATTTCAAATCCATCATCTCTTTA  
AATCCTGCCTCCTTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATG  
TTTACTCAATGTTTAAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT  
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGREFPMMHHHQAPSDGQT  
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILI  
ILHQ

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**FIGURE 303**

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCCTGGGTGCTCTTCATCTT  
 GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTTGGCCACTGAAACTCATCTGCTGCCAGTGTTAC  
 TGGATTATTCCTTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG  
 GGTGATTACAGTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT  
 AGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGGACATCTTATGC  
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA  
 AATCCGCCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG  
 AGGAGCCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG  
 AGCACAGAAGTGAAACACGTGACCAGGTAGAATGGATATTTTCAGGACGCGCGCAAAGGA  
 GGAGATTGTATTTTCGTTACTACCACAAACTCAGGATGTCTGTGGGAGTACTCCCAGAGCTGGG  
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATG  
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCT  
 GGTGTTCAAGAAAACCATTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACCTGGTGACCC  
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
 TGTGCCACAATCCTGCTGCTCCCTGTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA  
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG  
 AAAAACCCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA  
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA  
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGTGGGG  
 GAATGCCAAAAACACAGCAAGCCTTT**TGAGA**AGAATGGAGAGTCCCTTCATCTCAGCAGCGG  
 TGGAGACTCTCTCCTGTGTGTGTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC  
 CCAGCTGTCTCCTGTCTCATTTGTTGGTCAATACCTGAAGATGGAGAATTTGGAGCCTGG  
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT  
 GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA  
 AAAACCAACCCAAATCAA

**FIGURE 304**

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSSALMGCVFQSTEDKCIFKIDWTLSPG  
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY  
HKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGNLVFKKTIV  
LHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLPVLILIVKKTGKSSVNSTV  
LVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR  
SDRNSLEKKSGGGMPKTQQAF



**FIGURE 305**

CTATGAAGAAGCTTCTTGAAAAACAATAAGCAAAGGAAAAACAATGTGTCCCATCTCACATG  
GTTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG  
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA  
GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG  
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG  
ATGGTTGTGGGCTGGTGGCTCTGGGGATTGGTCTGTGCATGCAGCGCAATTACCTACAAGA  
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC  
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG  
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG  
AGTACATCAAAGCCAGGACTCATTTAATTCGTGGGTCGGATTATCTCGCCAGAAGTCGAAT  
GAGGCTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA  
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG  
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT  
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

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**FIGURE 306**

MQDEDGYITLNIKTRKPALVSVGPASSSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFRRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL  
EDGKGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

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**FIGURE 307**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG  
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCCAGTGC GGAGAA  
GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT  
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC  
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTCACCCAAAGTTCAAATTTGTGAGTACATTTACCAAACAAACAGG  
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

**FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498  
><subunit 1 of 1, 245 aa, 1 stop  
><MW: 27564, pI: 10.18, NX(S/T): 1  
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNLNVFSRVKLFSGSKRRRRRP  
EPQLKGIIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA  
MNSEGilytSELFtPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGlnKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSGVLNGGKSMShNESt

**N-glycosylation site.**

amino acids 242-246

**Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site.**

amino acids 93-100

**N-myristoylation site.**

amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

**HBGF/FGF family proteins**

amino acids 78-94, 102-153

**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG  
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCT  
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTG  
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCACACCCCTGTAGATTAC  
 AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA  
 ACCACGTCTTGGAATTTAGTGGGTCTTGCGCTTTGGGATAGGTGAAGTGAGGACAGACACTG  
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG  
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCT  
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGTCCCTGTGGGTGGGGCAG  
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG  
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGCTCCTCCCGGGGCGCT**ATG**GCGGCGCTGGC  
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCCGGGGGAGCCGGCCGGTGTGGG  
 CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAAGCAGCTCCTCATCCTG  
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGCCGGACCGCGGCCCGGAGCCTCA  
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCGGCCAGGGTTTCTACCTCCAGGCGAATCCCCG  
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT  
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC  
 TGAGGGACTGCTCTACAGTTCGCCGCAATTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT  
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC  
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA  
 GGCAGCTGCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
 ACAGTGTCCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG  
 GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGT

310/330

## **FIGURE 310**

MAALASSLIRQKREVREPGGSRPVS AQRRVCFRGTSKLCQKQLLILLSKVRLCGGRPARPDR  
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

### **Tyrosine kinase phosphorylation site:**

amino acids 199-207

### **N-myristoylation sites:**

amino acids 54-60, 89-95, 131-137

### **HBGF/FGF family signature:**

amino acids 131-155

310/330  
MAALASSLIRQKREVREPGGSRPVS AQRRVCFRGTSKLCQKQLLILLSKVRLCGGRPARPDR  
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

**FIGURE 311**

**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGGCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAACCAGTCAACAAGAGTAAGACAACA**TAG**

**FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKROAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR  
RQDPQLKGIVTRLYCRQGYLQMHDPGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY  
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR  
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT

**N-glycosylation site.**

amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site.**

amino acids 199-207

**N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins.**

amino acids 104-155, 171-198



GGGAGGAGGAANTGACCATGTAAAGAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAA  
GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA  
ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAAACAACAATGTGTATATGTGCACACAGGAGCATTCAAGAATG  
AAATAAACAGAGTTAGACCCGCGGGGGTGTGGTGTGTTCTGCACATAAAATAAATAATCTTAAAGCAGCTGTTCCC  
CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTCAATT  
TTCTCTATAAAGGAGAAAGTGAGCCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA  
AGAACTGGTGTGGTGCTTTTTCTTTCTTTTGAATTTCCCAACAGAGAGAGCAAAATTAATAATACATCTGCA  
AAAGAAATTTTCAGAGAAGAAAGTGTACCCGCGCAGATTGAGGCATGTGATTGGGGGAGAGAAACCGACAGACA  
CAGTTGGATTGTGCCTATGTGTACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT  
TTTTTAAATTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTTGTCTTAAACACCTGGATTCCATCT  
GGATGTGCTGTGATCAGTCTGAATCAACTGTTTGAATTCAGAAGGAACCAACACCATGATAAATATGAATG  
TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGCGCTATTTGACCCCT  
GCTTGTGGTGCTGCTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGT  
GCTCCTGCAGCAACCACTGTCAGCAAGTGATTGTGTTGCGAAAACCTGCGTGAGGTTCCGGATGGCATCTCC  
ACCAACACACCGCTGCTGAACCTCCATGAGAACCAAACTCCAGATCATCAAGTGAACAGCTTCAAGCATCTGAG  
CCTCTGGAAATCTTACAGTTGATGAGAACCATTGACGAACATTGAAATGGGGCTTTCAATGTGTGGCGA  
ACCTCAACACTCTGGAATCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGATACTTGTCTAAA  
CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAGGCATCCCTTCTTATGCTTTTAAACAGAATCCTTCTTT  
GCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTTGAAGGCTGTGCCACT  
TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAAACTAGATGAG  
CTGGATCTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAAT  
GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA  
ACCTGGCACAACAATAATCTAACATTGATGCTGACTGACCTTTCATCTGCTATCTAGAGGTCGATACAT  
TTACATCAACAACCTTTGGAATCTGTAATCTGCTCATATCTGGCTCAGCTGGTGGGATAAAAGACATGGCCCCCTC  
GAACACAGCTTGTGTGCCCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTATGGAGAGCTCGACCAGA  
ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCT  
GAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA  
TGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTCAAAATGTAATCTGTGCAAGATA  
CAGGCAITGTACACATGTATGGTGAGTAATCCGTTGGGAATAGTACTGCTCAGGCCACCTGAAATGTTACTGCA  
GCAACCACTACTCCTTTCTCTTACTTTTCAACCTGCAGTAGACTATGGAACCGTCTCAGGATGAGGCACG  
GACCAACAGATAAACAATGTGGGTCCCATCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC  
CACAAGCAGACAAGGTCGACAGAGAAAACCTTCACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAATT  
GATGAGGTCATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT  
GGTCATTTTCTACAAGATGAGGAAGCAGACCATCGGCAAAACCATCACGCCCAACAGGACTGTTGAAATTA  
TTAATGTGGATGATGAGATTAGGGGAGACACCCCATGGAAGGCCACCTGCCCATGCTGCTATCGAGCATGAG  
CACCTAAATCACTATAAATCAATCAAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCATACA  
CAGTTCAAGTGCATGAACGGTTATTGATCCGAATGAAGTCTAAAGACAATGTACAAGAGACTCAAACTTAAACA  
TTTACAGAGTTTACAAAAACAAACAATCAAAAAAAGACAGTTTATTAATAATGACACAATGACTGGGCTAA  
ATCTACTGTTTCAAAAAAGTGCTTTTACAAAAAACAACAAAAAGAAAAGAAATTTATTTATTAATAATTCATTG  
TGATCTAAAGCAGAAAAA

**FIGURE 314**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
 VRKNLREVPDGIENTRLLNLHENQIQIIVNSFKHLRHLLEILQLSRNHIRTIEIGAFNGLA  
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
 YISEGAFEGLSNLRYNLAMLNREIPNLTPLIKLELDLSEGNHLSAIRPGSFQGLMHLQKL  
 WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHHPWNCNCIL  
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
 LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTVQDTGMYTCMVNSVGN  
 TTASATLNVTAATTTFFSYFSTVTVETMEPSQDEARTDNNVVGTPVVDWETTNVTTSLTPQ  
 STRSTKFTTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
 HHAPTRTVEIINVDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
 VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
 434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
 391-397, 422-428, 433-439, 531-537

CGCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCCGCACAT  
GGCTGCAGCCACCTTCGCGCGCACCCGAGGCGCGCGCCAGCTCGCCCGAGTCCCGTCGGA  
GGCGCCCGGCCGCCCGGAGCCAAAGCAGCAACTGAGCGGGAAGCGCCCGCTGCGGGGATC  
GGGATGTCCTCTCTCTCTCTCTCTCTGCTAGTTTCTCTACTATTGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGTGCAGAGGAAAAGGTCATTGCGCTGCCACCATCAACTGGGGG  
TTCAGAAAAAGACACTTGGATATTGAATGGCTGCTCACCATAAGAGGAAACAAAAA  
GTGGTGATCACTTACTCCAGTCGTCATGCTACAAATACTTACTGAGGAACAGAAGGGCC  
AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTTGAAG  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGATTTCAGGCGGCTAGCTGTGGAGCCAT  
GTCATCTTAAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTAGTTGGAAGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGTCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT  
ACTGCGCAGCGAATCCGAGAGAAAGAGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATT  
GACTACAACACCCTGGACAGAGTTCTGCTGCAGAATCTTACCATTGCTCTCTGAGATTGTA  
CCAGTGCACAGAGCCGCAAGAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAAGTGTACAGT  
ATGTACAAAGCATCGCATGGTTGCAGGAGCAGTGCAGGCATAGTGGCTGGAGCCCTGCTG  
ATTCTTCTCTTGGTGTGGCTGAATCCGAAGGAAGACAAAGAAGATAGAGGAAGA  
GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCAAAGGCCGTCTGTGAAACCGAGCT  
CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTGGTTCTTCTCTCACTGCGCTCCACAGAACAT  
AGTGCTTCAGCAGCGGACGGGACATCTCAACTGACGCGACCCAGCCAGGGCTGGCCAC  
CCAGGACATACGCTAGTGGGCGAGAGTGTAGAGGTTCTGAAACCAAAGAAAGTCCACAT  
CTAATCTGACCAAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGACCTTCCAA  
ACGGTCTGCAATTACAAATGGAATGACTCCACCGTTTCCTAGGATCAGGGCTTTTGGACT  
TTCTCGTCATTGGAGCTCAAGTCACCGCCACACAACCAAGTGAAGTCAATTAAGTAGCA  
GTGAGCATTCAGCCAGGAACGATTCCAGTAGGCAATTTCTCTATACAATACCAAAACAGCAA  
AGGATGTAAGCTGATTCTATCTGTA AAAAGGCATCTTATTGTGCCTTTAGACAGAGTAAGG  
AAAGCAGGAGTCCAAATCTATTTTGTTGACCAAGGACCTGTGGTGAGAAGTTGGGGAAAGTG  
AGGTGAATATTACATAAACTTTTAATGTGGGATATTGTTATCAGTGCTTTGATTACAAAT  
TTCAAGAGGAAATGGGATGCTGTTTGAATAATTTTCTGATCATTTCGCAAACTTATTGGATT  
ATTAGTTATTTCAGACAGTCAAGCAGAAACCCAGCCCTATTACACCTGTCTACACCTGTAC  
TGAGCTTAACCATCTTAAGAAACTCAA AAAAGGAAACATGTGTCTTCTTATTGCTACTTAAC  
TTCATTGTGCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAAATGAGTTTCTCCCACTATACATAATCTCACTATTGTTGATTGAGCCCCAAAATAAC  
TATGAAAGGAGACAAAATTTGTGCAAAAGGATTTGTGAAGAGCTTTCCATCTTCTATGATTG  
ATTGAGGATTGTTGACAAACATTAGAAATATATATAATGGAGCAATTTGTGGATTTCCCTTCAAT  
CAGATGCCTCTTAAGGACTTTCTCTGTAGATTATTTCTGGAAGGAGAAAATACACATGCTATT  
TATCAACGCTCTTAGAAAGAATTTCTCTAGAGAAAAGGATCTAGGAATGCTGAAAGATT  
CCCAACATACATTATAGTCTCTTCTTCTTGTGAAAATGTGAAACCAGAAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATAGTTTCTCTTGAATATTGTCAAGGAAGGTACCGGGCA  
TGGTGCCAGGCCTGTAGGAAAATCCAGCAGGTGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCAGCCTGGGTGACAGAGCGGAGCTCGTCTC

316/330

## **FIGURE 316**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

**FIGURE 317**

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCGAGCCGCGCCACGGCACGGCAGCCCA  
 CCATGGCGCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGAGTTTCGCCAGAGTTTGAGTATCACTACT  
 CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCTATCGCCATGCAAAATTTACGCTTAGTCCCAGAA  
 CCAGGAGCCGCTGGACATCGAGTGGCTGATATCACAGCTGATAATCAGAAAGTGATCAAGTGATTATTTTAT  
 ATCTCGGAGACAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC  
 AAATCTGGTGATGCATCAATAAATGTAAAGATTTACAACGTGTCAGATATTGGCAGATATCAGTGCAAAAGTAA  
 AAAAGCTCCTGGTGTTCGAAATAAGAAGATTCATCTGGTAGTTCTTGTGTAAGCCTTCAGGTGCGAGATGTTACG  
 TTGATGGATCTGAAGAAATGGAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATTACAG  
 TATGAGTGGCAAAATTTGCTGACTCACAGAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT  
 ATCTGTAAGAAATGCCTCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC  
 AGTGCCTGTTGCGTCTAAACGTTGTCCTCCTTCAATAAAGCTGGACTAATTCAGGAGCCATTATAGGAACT  
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTGCTGTGCTGTAAGGCGCAGAGAGAAATAATGAAAA  
 GGAAGTTCATCAGATATCAGGAAGATGTGCCACCTCCAAGAGCCGTACGTCCTACTGCCAGAGCTACATCG  
 GCAGTAATCATTCATCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATTCAGAGCTCAGTATAACCAA  
 GTACCAAGTGAAGACTTTGAACGCATCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCTTACAA  
 GACTGATGGAATTACAGTTGATTAATATGAGTACTGAAGATCTGAAGTATGTATTTATTTGACTTTATTTT  
 AGGCCTCTAGTAAAGACTTAATGTTTTTAAAAAAGCACAGGCACAGAGATTAGAGCAGCTGAAGAACAC  
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCAATGTCAAATTAGTACAGGCCAAATCTTTGT  
 TAAAAACCCCTATGTATAGTGACACTGATAGTAAAAAGATGTTTTATTTATTTTCAATAACTTACCCTAACAA  
 .ATTTTTAACTTTTCATATGCATATTCGTATATGTGGCTTTTAGGAAAAGTAGGTTAATAGTTGATTTTTCAA  
 AGGAAATTTAAAAATTTCTACGTTCTGTTTAATGTTTTGCTATTTAGTTAAATACATTGAAGGAAAATACCCG  
 TTCTTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTGTCGCTCAAACTATTTTATTTGCAACTACA  
 TGATTTCACACAATCTCTTAAACAACGACATAAAATAGATTTCTTGTATATAAATAACTTACATACGCTCCA  
 TAAAGTAAATTCCAAAGTGCTAGAACAAATCGTCCACTTCTACAGTGTTCTCGTATCCACAGAGTTGATGC  
 ACAATATATAAATACTCAAGTCCAAATATTAATAAATCTAGGCACCTTGACTAACTTTAATAAATTTCTCAAAC  
 TATCAATATCTAAAGTGATATATTTTTTAAAGAAAGATTATCTCAATAACTTCTATAAAAAAAGTTTGATGG  
 TTTGGCCCATCTAACTTCACTACTATTAGTAAGAACTTTAACTTTTAAATGTGTAGTAAGGTTTATCTACCTT  
 TTCTCAACATGACACCAACAACTCAAAAACGAAGTTAGTGAGGTGCTAACATGTGAGGATTAACTCCAGTAT  
 TCCGGTCACAATGCATTCAGGAGGAGGTACCCATGTCACTGGAATTGGGCGATATGTTTATTTTTTCTTCCC  
 TGATTTGGATAACCAATGGAACAGGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTCCTGGCTT  
 TTTCTGGGCAAGGGTGCCACATTTGAAGAGGTGGAAATATAAGTTCTGAAATCTGTAGGGAAGAGAACAT  
 TAAAGTTAATTCAGAGGAAAAATCATCATCTATGTCCAGATTTCTCATTTAAAGACAAAGTTACCCACAACACT  
 GAGATCACATCTAAGTGACACTCCTATTGTGAGTCTAAATACATTTAAAAACCTCATGTGTAATAGCGGTATAA  
 TGTATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAATCAAAACAGTACTTCTTAAACAA  
 CTTCAACCAAAAAAGACCAAAACATGGAACGAATGGAAGCTTGAAGGACATGCTTGTGTTTAGTCCAGTGGTTT  
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAACATTTGAGGCTGGAGGCCATTATCCTT  
 AGCAACTAATGCAGAAACAGAAAAATCACTACCGCATGTTCTCACTTATAAGTGGGAGGTAAATGATAAGAACT  
 TATGAACCAAAAGAGGAAACATAGACATTTGGAGTCTATTTGAGAGGGGAGGGTGGGAGAGGAAAAGGAGCA  
 GAAAAGATAACTATTGAGTACTGCCTTACACCTGGGTGATGAATAATATGTACACAAATCCCTGTGACACA  
 GTTTTACCTATGGAACAAACCTTCATGTGATCCCTAAACCTAAAATAAAGTTAAAAAATAAATAAATAAATAA  
 AA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 318**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFAFSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA  
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK  
APGVANKKIHLVVLVKPSGARCIVDGSSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT  
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL  
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM  
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

**Signal sequence.**

amino acids 1-19

**Transmembrane domain:**

amino acids 236-257

**N-glycosylation sites.**

amino acids 106-110, 201-205, 298-302

**Tyrosine kinase phosphorylation sites.**

amino acids 31-39, 78-85, 262-270

**N-myristoylation sites.**

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302

**Myelin P0 protein.**

amino acids 96-125

**FIGURE 319**

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA  
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC  
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC  
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC  
 CTTTGTGCGGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG  
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT  
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
 GCTGAGAGCTGTTACCTTGTCACACCCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA  
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACT  
 TTGTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
 AGTGACACAGGCGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC  
 TCTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC  
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCA  
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT  
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACTCTATTT  
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG  
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG  
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT  
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAAGTGAAGTTCAGAGCATGAAAATCACACT  
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGAAGG  
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT  
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT  
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA  
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 320**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQLQSLWTLARPFCPPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVK  
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH  
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL  
TKALGEVDILLTWMQKFYKL

**Signal sequence:**

amino acids 1-42

**N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130



**FIGURE 321**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA  
TCAGGAGCCAAACCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC  
CACTGGCTGCGCTCAGGCTGTCTTATTCGCTTGAAAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGCCTGCAGGCCATCCTGGGAGTAAAGGCTGCCTT  
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

**FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST  
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ  
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT  
 AGAATAACATCCACTTTGCCCTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTC  
 GGTTCATATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG**ATGT**TGGGGGCCCGCCT  
 CAGGCTCTGGGTCTGTGCCCTGTGTCAGCGTCTGCAGCATGAGCGTCCCTCAGAGCCTATCCCA  
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC  
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
 TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTGGATCACACTATTTTCGAC  
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC  
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC  
 CACCCCGTACTCCCGATTCTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC  
 CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT  
 GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGGCCTCCTGTTACAGGAGCTCCCGAGCG  
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAAC  
 ACGCAGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATC**TAG**GGTCTG  
 CTGG

**FIGURE 324**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD  
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENG  
DVYHSPQYHFLVSLGRAKRAFLPGMNPPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSE  
RDPLNVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA  
KFI

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

**FIGURE 325**

GGTGAAGGAGTACCCGCGAGAGACAGCCAGCAGTCTTGTGGAGGACAGCGGTGCCCGGCTAGC**ATG**  
GGTGTCTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGTGAG  
ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA  
GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTGC  
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGAC  
ACAGTTCAGACCATCACAGGCAGTGATCCCAGGAAGCCATCTTTGACACCTTTGCACCGA  
TGACAGCTCTGAAGAGGCAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC  
ACCCCGTCAAGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCC  
GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT  
GGTCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG  
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCAGCATCCCTGGGGCTCAGA  
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACCAGCTCTGC  
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC  
ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA  
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA  
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGAGTGGGCAAAACAACCTT  
CTTTGCTGGGAGCTCTGCTTCTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC  
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACACAGAGGGACCCCT  
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC  
GAGGCCGACCACAGACG**TGAG**TGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG  
TGGCTTCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
CGGGAACCTCACGCCCACGCGCTCACTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA  
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG  
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGACCCCTCGCTCACATCCAC  
CGGAGTGATGTATGGGGAGGGGCTTCACTGTTFCCAGAGGTGCTTGGACTCACCTTGG  
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA  
TTAAATTTCACTCAGTGTGGCCCCAAAAAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL  
 ETSSRASTPAGPIPEAETRGAKRISPARETRSF TKTS PNF MVLIATSVETSAASGSPEGAGM  
 TTVQTITGSDPEEAI FDTLCTDDSS EEA KTLTMDILT LAHTSTEAKGLSSESSASSD GPHPV  
 ITPSRASESSASSD GPHPVITPSRASESSASSD GPHPVITPSWSPGSDVTL LAEALVTVTNI  
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL  
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETSALS VETPSY  
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGFFPTSRD  
 PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP-and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

**FIGURE 327**

GCGGAGCATCCGCTGCGGTCTTCGCCGAGACCCCCGCGGGATTGCGCGGTCTTCCCGCGG  
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA  
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATTAAGACCAGAGGGGAGGATTAT  
 CTTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG  
 CTTGACTTACACTTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCCTTGCTGTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAAACCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC  
 TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA  
 TAGCTCATCTGCTGCTGAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATAACACCTCGGCTACTCCAAGGCCGCCACCCCTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGACTCGAAAGGCAGCTTAGA  
 AACCATAACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCCTA  
 CTGCACCTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGGTGATAGGCC  
 TCGTCTCTCTGGGTAGAATCTTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
 TAGTAACCGAAGCCCAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAATGCCCTTCTGCTTTCTCTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
 CTGGGTTCAAGCGATTCTCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTCCACATGTTGGTCAGGCTG  
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGGAATGAAGTG  
 GAAACCAATTAGGTAATTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT  
 ATGTAAAGTAATAAGTATAATTGCCATATAAATTTCAAAATTCAACTGGCTTTTATGCAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCCTGGTTCCAGATAAAATCAAC  
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTTATATGGATTTCCTTTAAACCTATT  
 CCAGATGTAGTTCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

**FIGURE 328**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSESLLRRKRYSRLDYLINGIYVDI
```

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321



**FIGURE 329**

CTCCACGGTGTCCAGCGCCAGAAATGCGGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
 CCTGTCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGTT  
 GGGATCCTCTTCTCTCGTCTGCTCTGGCACCCTATATGCAGAGAAGAGGCGAGGACCAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTTCGAAAAACGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCTCCTCCCTCCCTTCTCCAC  
 CTTCAGCCTCTGGCTACAACACGCTGACGCCCAAGGCAAAAGCTCAGCAAAACCAGCACC  
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGAGGGAGCTCCCGCCCCCATGTCAGC  
 TGGACTCCACCTCAGCAGAGGACACCAAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG  
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTCTGAGCCTTCTGTTCAGC  
 CGCAGGCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAAGGAAGCC  
 CCTTCCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA  
 TCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCAACCTCCCAAGGCTCTCCTCTGTCATGTTCCA  
 GCCTGACCTAGAAGCGTTTTGTAGCCCTGGAGCCAGAGCGGTGGCCTTGTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGTTTACATCCCTGGGCAGAGTACCAGGCTGTGACCCCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC  
 CTCATGCCAGTGTCTGGACCCTGCCTTCTCCTCCACTCCAGACCCCACTTGTCTTCCCTCCC  
 TGGCGCTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
 GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACCAAAACATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTTCTAACAAATGCCAGTGACTGTGCACCTTGAAGTTTGAAGGCCAGTGGGCCG  
 ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACCTGCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCAGTGGGGACTCCCCTGAGGCCCTGCTAAG  
 TCCAGGCTTGGTGCAGTCCAGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG  
 TTGCCTTTNCCATTGTGCCCTCCCTGGNCCATGCCTTCTGCTCTTGGCAAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCCCTTGTCTGGAAGGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA  
 GAAAAGTAGAAAACAGAGTGACGCTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGGCCCTGGAGAGGGGTGCGGGGTGGTGGTAAAGTA  
 GCACAACCTACTATTTTTTTCTTTTCCATTATATTGTTTTTAAGACAGAATCTCGTGTCT  
 GCTGCCACGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGGCTCCTGGGTTCAAGTGATT  
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCAACCAACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
 CTCAAATGAGCCTCCTGCTTCACTCTCCCAATTGCCGGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTTAAAGTGAATTAAGAGTTGTTCAGTATGCAAACTTGGAAAG  
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTACCCATAGTCTCACCAGAGACTATCAT  
 TATTTCTGTTTTTGTGTTACTTCTTCCACTCTTTCTTCTTACATAAATTTGCCGGTGTCTCT  
 TTTACAGAGCAATTAATCTGTATATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
 ATCACTTTATTCAGCACTTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCVEKRGPDSELLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD  
VISMPPLHTSEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128